GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 4, 2004, 16:42:49 ; Search time 155 Seconds
(without alignments)
833.178 Million cell updates/sec

Title: US-10-763-972-2
Perfect score: 1936
Sequence: 1 MLSILLPSRGSRSGSRRGAL.....QNKLGEHPAGRKRCPGLNRS 360

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1936	100.0	360	5	ABB98145	Abb98145 Human GPC
2	1936	100.0	361	7	ADB99264	Adb99264 Human p2Y
3	1798	92.9	333	4	AAG64125	Aag64125 Human G p
4	1542	79.6	295	5	AAU11251	Aau11251 Human P2Y
5	1529	79.0	361	5	ADI16630	Adi16630 Human NOV
6	1519	78.5	361	8	ADN42284	Adn42284 Human nov
7	1189	61.4	338	7	ADC26009	Adc26009 Human pur
8	1189	61.4	338	7	ABW00804	Abw00804 Human GPC
9	1185	61.2	339	5	ABB98146	Abb98146 Human GPC
10	1185	61.2	339	5	AAE18640	Aae18640 Human G-p
11	1185	61.2	339	8	ADO30394	Ado30394 Human GPC
12	1179	60.9	338	7	ADC26000	Adc26000 Human pur
13	942	48.7	271	7	ADC86167	Adc86167 Human GPC
14	921	47.6	170	4	AAG80935	Aag80935 Human nGP
15	921	47.6	170	5	ABG93753	Abg93753 Human G p
16	785	40.5	302	8	ADO30396	Ado30396 Mouse GPC
17	447	23.1	328	5	ADI16984	Adi16984 NOVX prot
18	447	23.1	328	5	ADI16983	Adi16983 NOVX prot
19	447	23.1	328	8	ADP49191	Adp49191 Chick P2y
20	421	21.7	374	4	AAE04390	Aae04390 Turkey P2
21	421	21.7	374	5	ADI16982	Adi16982 Turkey NO
22	416	21.5	537	5	AAU74538	Aau74538 Human P2Y
23	416	21.5	537	5	ADI16981	Adi16981 Human NOV
24	400	20.7	328	7	ADD45304	Add45304 Rat Prote
25	395	20.4	328	2	AAR91224	Aar91224 Mouse pan
26	395	20.4	328	7	ADC37339	Adc37339 Nuclear f
27	395	20.4	328	8	ADO29601	Ado29601 Mouse GPC
28	394.5	20.4	377	4	AAE01144	Aae01144 Human pur
29	392.5	20.3	328	2	AAR91225	Aar91225 Human pla
30	388	20.0	361	5	ADI16985	Adi16985 Rat NOVX
31	388	20.0	361	7	ADH69290	Adh69290 Rat orpha
32	388	20.0	361	8	ADF91782	Adf91782 Rat orpha
33	387.5	20.0	328	4	AAE04393	Aae04393 Human P2-
34	387.5	20.0	328	6	ABP81869	Abp81869 Human pur
35	387.5	20.0	328	7	ADC37341	Adc37341 Nuclear f
36	387.5	20.0	328	7	ADD45306	Add45306 Human Pro
37	387.5	20.0	328	7	ADE38349	Ade38349 Human pro
38	387.5	20.0	328	7	ADN39970	Adn39970 Cancer/an
39	387.5	20.0	328	8	ADO29600	Ado29600 Human GPC
40	387.5	20.0	328	8	ADP49195	Adp49195 Human P2Y
41	387.5	20.0	377	4	AAE01143	Aae01143 Human pur
42	387.5	20.0	377	4	AAE04392	Aae04392 Human P2-
43	387.5	20.0	377	6	ABP81866	Abp81866 Human pur
44	387.5	20.0	377	7	ADE62766	Ade62766 Human Pro
45	387.5	20.0	377	8	ADO29596	Ado29596 Human GPC

ALIGNMENTS

RESULT 1
ABB98145
ID ABB98145 standard; protein; 360 AA.
XX
AC ABB98145;
XX
DT 17-OCT-2002 (first entry)
XX
DE Human GPCR designated PFI-020.
XX
KW Human; GPCR; G-protein coupled receptor; antidepressant; neuroleptic;
KW gene therapy; therapeutic; mood; depression; arousal; eating; sleeping;
KW disorder; PFI-020.
XX
OS Homo sapiens.
XX
PN EP1215214-A1.
XX
PD 19-JUN-2002.
XX
PF 04-DEC-2001; 2001EP-00310137.
XX
PR 18-DEC-2000; 2000GB-00030855.
PR 17-JAN-2001; 2001GB-00001222.
XX
PA (PFIZ) PFIZER LTD.
PA (PFIZ) PFIZER INC.
XX
PI Fidock MD;
XX
DR WPI; 2002-510798/55.
DR N-PSDB; ABQ76000.
XX
PT New polynucleotide encoding G protein-coupled receptor PFI-020, useful
PT e.g. for treating eating and sleeping disorders and for identifying
PT specific modulators.
XX
PS Claim 1 (a); Page 11-12; 23pp; English.
XX
CC The invention relates to an isolated polynucleotide encoding a novel
CC polypeptide belonging to the class of proteins known as G-protein coupled
CC receptors (GPCRs). The activity of proteins of the invention may be
CC described as, antidepressant and neuroleptic. Polynucleotides of the
CC invention are used for recombinant expression of the G protein-coupled
CC receptor (PFI-020) polypeptides, to create transgenic animals, as source
CC of primers, probes, antisense sequences and ribozymes and in gene
CC therapy. Therapeutic agents of the invention can be used to treat a wide
CC range of disorders, particularly mood disorders, depression or arousal,

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CC   especially eating and sleeping disorders. The current sequence represents
CC   a human GPCR designated PFI-020
XX
SQ   Sequence 360 AA;

  Query Match           100.0%;  Score 1936;  DB 5;  Length 360;
  Best Local Similarity  100.0%;  Pred. No. 5e-207;
  Matches  360;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLSILLPSRGSRSGSRRGALLLEGASRDMEKVDMNTSQEQGLCQFSEKYKQVYLSLAYSI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLSILLPSRGSRSGSRRGALLLEGASRDMEKVDMNTSQEQGLCQFSEKYKQVYLSLAYSI 60

Qy         61 IFILGLPLNGTVLWHSWGQTKRWSCATTYLVNLMVADLLYVLLPFLIITYSLDDRWPFGE 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 IFILGLPLNGTVLWHSWGQTKRWSCATTYLVNLMVADLLYVLLPFLIITYSLDDRWPFGE 120

Qy        121 LLCKLVHFLFYINLYGSILLLTCISVHQFLGVCHPLCSLPYRTRRHAWLGTSTTWALVVL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLCKLVHFLFYINLYGSILLLTCISVHQFLGVCHPLCSLPYRTRRHAWLGTSTTWALVVL 180

Qy        181 QLLPTLAFSHTDYINGQMIWYDMTSQENFDRLFAYGIVLTLSGFLSLLGHFGVLFTDGQE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 QLLPTLAFSHTDYINGQMIWYDMTSQENFDRLFAYGIVLTLSGFLSLLGHFGVLFTDGQE 240

Qy        241 PDQARGEPHEDRQHSPSQVHPDHPTGVWPLHPLFCALPYHSLLLPHHLLSAFSGLPALDG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 PDQARGEPHEDRQHSPSQVHPDHPTGVWPLHPLFCALPYHSLLLPHHLLSAFSGLPALDG 300

Qy        301 SQCGLQDMEASGECEQLPQPSPVLSFKGGKNRVRLLQKLRQNKLGEHPAGRKRCPGLNRS 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 SQCGLQDMEASGECEQLPQPSPVLSFKGGKNRVRLLQKLRQNKLGEHPAGRKRCPGLNRS 360


RESULT 2
ADB99264
ID   ADB99264 standard; protein; 361 AA.
XX
AC   ADB99264;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Human p2Y2li protein.
XX
KW   gene; human; P2Y2li; chromosome 3; G protein-coupled receptor; GPCR;
KW   Class A rhodopsin-like sub-family; gene therapy; receptor.
XX
OS   Homo sapiens.
XX
PN   DE10144044-A1.
XX
PD   27-MAR-2003.
XX
PF   07-SEP-2001; 2001DE-01044044.
XX
PR   07-SEP-2001; 2001DE-01044044.
XX
PA   (BRUE/) BRUESS M.
PA   (BOEN/) BOENISCH H.
PA   (VKUE/) VON KUEGELGEN I.
XX
PI   Bruess M,  Boenisch H,  Von Kuegelgen I;
XX
DR   WPI; 2003-364675/35.
DR   N-PSDB; ADB99267.
XX
PT   New human gene P2Y2li and encoded G protein-coupled receptor, useful for
PT   treatment and diagnosis of receptor-associated diseases and for drug
PT   screening.
XX
PS   Disclosure; Page 4; 6pp; German.
XX
CC   This invention describes the human P2Y2li gene and its 5'- and 3'-
CC   untranslated regions, located on chromosome 3 which is a novel G protein-
CC   coupled receptor (GPCR). The protein encoded by P2Y2li is expressed in
CC   blood cells, testis and embryonal kidney cells and contains potential
CC   sites for phosphorylation by protein kinase C and casein kinase II. It is
CC   a member of the Class A rhodopsin-like sub-family of G protein-coupled
CC   receptors and it probably a nucleoside/nucleotide receptor that mediates
CC   action of nucleosides/nucleotides or their sugar derivatives. P2Y2li and
CC   antibodies directed against the encoded protein are useful in diagnosis
CC   and treatment (including gene therapy) of diseases associated with
CC   abnormal levels of P2Y2li expression, in screening assays for modulators,
CC   potential therapeutic agents, and to produce transgenic animals, e.g. for
CC   identifying diseases associated with abnormal expression of P2Y2li. This
CC   sequence represents the human P2Y2li protein described in the disclosure
CC   of the invention.
XX
SQ   Sequence 361 AA;

  Query Match           100.0%;  Score 1936;  DB 7;  Length 361;
  Best Local Similarity  100.0%;  Pred. No. 5.1e-207;
  Matches  360;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLSILLPSRGSRSGSRRGALLLEGASRDMEKVDMNTSQEQGLCQFSEKYKQVYLSLAYSI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLSILLPSRGSRSGSRRGALLLEGASRDMEKVDMNTSQEQGLCQFSEKYKQVYLSLAYSI 60

Qy         61 IFILGLPLNGTVLWHSWGQTKRWSCATTYLVNLMVADLLYVLLPFLIITYSLDDRWPFGE 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 IFILGLPLNGTVLWHSWGQTKRWSCATTYLVNLMVADLLYVLLPFLIITYSLDDRWPFGE 120

Qy        121 LLCKLVHFLFYINLYGSILLLTCISVHQFLGVCHPLCSLPYRTRRHAWLGTSTTWALVVL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLCKLVHFLFYINLYGSILLLTCISVHQFLGVCHPLCSLPYRTRRHAWLGTSTTWALVVL 180

Qy        181 QLLPTLAFSHTDYINGQMIWYDMTSQENFDRLFAYGIVLTLSGFLSLLGHFGVLFTDGQE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 QLLPTLAFSHTDYINGQMIWYDMTSQENFDRLFAYGIVLTLSGFLSLLGHFGVLFTDGQE 240

Qy        241 PDQARGEPHEDRQHSPSQVHPDHPTGVWPLHPLFCALPYHSLLLPHHLLSAFSGLPALDG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 PDQARGEPHEDRQHSPSQVHPDHPTGVWPLHPLFCALPYHSLLLPHHLLSAFSGLPALDG 300

Qy        301 SQCGLQDMEASGECEQLPQPSPVLSFKGGKNRVRLLQKLRQNKLGEHPAGRKRCPGLNRS 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 SQCGLQDMEASGECEQLPQPSPVLSFKGGKNRVRLLQKLRQNKLGEHPAGRKRCPGLNRS 360


RESULT 3
AAG64125
ID   AAG64125 standard; protein; 333 AA.
XX
AC   AAG64125;
XX
DT   25-SEP-2001  (first entry)
XX
DE   Human G protein-coupled receptor GPRv71.
XX
KW   Human; guanosine triphosphate binding protein-coupled receptor;
KW   G protein-coupled receptor; GPRv8; GPRv12; GPRv16; GPRv21; GPRv40;
KW   GPRv47; GPRv51; GPRv71; GPRv72; cancer; liver cirrhosis;
KW   Alzheimer's disease; cytostatic; hepatotropic; nootropic;
KW   neuroprotective; gene therapy; peptide therapy.
XX
OS   Homo sapiens.
XX
PN   WO200148188-A1.
XX
PD   05-JUL-2001.
XX
PF   28-DEC-2000; 2000WO-JP009408.
XX
PR   28-DEC-1999;   99JP-00375152.
PR   31-MAR-2000; 2000JP-00101339.
XX
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PA (HELI-) HELIX RES. INST.
XX
PI Matsumoto S, Oda T, Saito Y, Morikawa N, Yoshida K, Suwa M;
PI Sugiyama T, Kishimoto T, Kanzaki K, Yasuda S, Inoue Y;
XX
DR WPI; 2001-425662/45.
DR N-PSDB; AAH73516.
XX
PT New DNA encoding guanosine triphosphate binding protein coupled receptors
PT and their expression products for screening potential anticancer and
PT nootropic drugs and in diagnosis of these diseases.
XX
PS Example 1; Page 132-135; 170pp; Japanese.
XX
CC The invention relates to nine human guanosine triphosphate binding
CC protein (G protein)-coupled receptors designated GPRv8, GPRv12, GPRv16,
CC GPRv21, GPRv40, GPRv47, GPRv51, GPRv71 and GPRv72, and to the genes
CC encoding them. These genes and proteins and antibodies against the
CC protein are useful in the treatment, prevention, diagnosis and
CC investigation of diseases associated with G protein-coupled receptors,
CC including cancer, cirrhosis of the liver and Alzheimer's disease. The
CC present sequence is a G protein-coupled receptor of the invention
XX
SQ Sequence 333 AA;

Query Match 92.9%; Score 1798; DB 4; Length 333;
Best Local Similarity 99.7%; Pred. No. 1.2e-191;
Matches 331; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy         29 MEKVDMNTSQEQGLCQFSEKYKQVYLSLAYSIIFILGLPLNGTVLWHSWGQTKRWSCATT 88
              ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db          1 MEKVDMNTSQEQGLCQFSEKYKQVYLSLAYSIIFILGLPLNGTVLWHFWGQTKRWSCATT 60

Qy         89 YLVNLMVADLLYVLLPFLIITYSLDDRWPFGELLCKLVHFLFYINLYGSILLLTCISVHQ 148
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YLVNLMVADLLYVLLPFLIITYSLDDRWPFGELLCKLVHFLFYINLYGSILLLTCISVHQ 120

Qy        149 FLGVCHPLCSLPYRTRRHAWLGTSTTWALVVLQLLPTLAFSHTDYINGQMIWYDMTSQEN 208
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FLGVCHPLCSLPYRTRRHAWLGTSTTWALVVLQLLPTLAFSHTDYINGQMIWYDMTSQEN 180

Qy        209 FDRLFAYGIVLTLSGFLSLLGHFGVLFTDGQEPDQARGEPHEDRQHSPSQVHPDHPTGVW 268
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FDRLFAYGIVLTLSGFLSLLGHFGVLFTDGQEPDQARGEPHEDRQHSPSQVHPDHPTGVW 240

Qy        269 PLHPLFCALPYHSLLLPHHLLSAFSGLPALDGSQCGLQDMEASGECEQLPQPSPVLSFKG 328
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 PLHPLFCALPYHSLLLPHHLLSAFSGLPALDGSQCGLQDMEASGECEQLPQPSPVLSFKG 300

Qy        329 GKNRVRLLQKLRQNKLGEHPAGRKRCPGLNRS 360
              ||||||||||||||||||||||||||||||||
Db        301 GKNRVRLLQKLRQNKLGEHPAGRKRCPGLNRS 332
```

RESULT 4
AAU11251
ID AAU11251 standard; protein; 295 AA.
XX
AC AAU11251;
XX
DT 26-FEB-2002 (first entry)
XX
DE Human P2Y-like G protein-coupled receptor.
XX
KW Human; P2Y-like G protein-coupled receptor; GPCR; COPD;
KW chronic obstructive pulmonary disease; nervous system disease;
KW Parkinson's disease; multiple sclerosis; dementia; stroke;
KW Alzheimer's disease; benign prostatic hyperplasia; urinary incontinence;
KW bacterial infection; fungal infection; protozoan infection;
KW viral infection; pain; cancer; anorexia; bulimia; asthma;
KW acute heart failure; hypotension; hypertension; osteoporosis; diabetes;
KW angina pectoris; myocardial infarction; ulcer; inflammation; allergy;
KW psychotic disorder; neurological disorder; anxiety; schizophrenia;
KW manic depression; delirium; severe mental retardation; dyskinesia.
XX
OS Homo sapiens.
XX
PN WO200185764-A2.
XX
PD 15-NOV-2001.
XX
PF 09-MAY-2001; 2001WO-EP005244.
XX
PR 11-MAY-2000; 2000US-0203582P.
PR 21-FEB-2001; 2001US-0269857P.
XX
PA (FARB) BAYER AG.
XX
PI Ramakrishnan S;
XX
DR WPI; 2002-075242/10.
DR N-PSDB; AAS17746.
XX
PT New polynucleotides for producing P2Y-like G protein-coupled receptors
PT (GPCR) that are used for screening inhibitors or regulators of human P2Y-
PT like GPCR, especially useful for treating pain, cancer or neurological
PT disorders.
XX
PS Claim 25; Fig 2; 114pp; English.
XX
CC The invention relates to an isolated polynucleotide encoding a P2Y-like G
CC protein-coupled receptor (GPCR) polypeptide, its fragment, derivative or
CC allele, a host cell containing an expression vector comprising the
CC polynucleotide and screening for agents that regulate the GPCR activity.
CC The polynucleotide is useful for producing P2Y-like GPCR polypeptide,
CC which may be employed for screening agents that inhibit or regulate human
CC P2Y-like GPCR. The reagent or inhibitor of the human P2Y-like GPCR is
CC useful for treating or ameliorating P2Y-like GPCR disorders, particularly
CC COPD (chronic obstructive pulmonary disease), peripheral or central
CC nervous system disease (e.g. Parkinson's disease, multiple sclerosis,
CC dementia, stroke, Alzheimer's disease and many other diseases and
CC disorders listed in the specification), benign prostatic hyperplasia or
CC urinary incontinence. A pharmaceutical composition containing the
CC modulators and/or regulators of P2Y-like GPCR is useful for modulating
CC the activity of a P2Y-like GPCR. In particular, these are useful for
CC treating, preventing or ameliorating infections (e.g. bacterial, fungal,
CC protozoan or viral infections), pain, cancer, anorexia, bulimia, asthma,
CC acute heart failure, hypotension, hypertension, osteoporosis, diabetes,
CC angina pectoris, myocardial infarction, ulcers, inflammation, allergies,
CC psychotic or neurological disorders (e.g. anxiety, schizophrenia, manic
CC depression, delirium, severe mental retardation or dyskinesias). The
CC present sequence is the P2Y-like GPCR of the invention
XX
SQ Sequence 295 AA;

Query Match 79.6%; Score 1542; DB 5; Length 295;
Best Local Similarity 98.6%; Pred. No. 4e-163;
Matches 284; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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Qy         29 MEKVDMNTSQEQGLCQFSEKYKQVYLSLAYSIIFILGLPLNGTVLWHSWGQTKRWSCATT 88
              ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db          1 MEKVDMNTSQEQGLCQFSEKYKQVYLSLAYSIIFILGLPLNGTVLWHSWGQTKRWSCATT 60

Qy         89 YLVNLMVADLLYVLLPFLIITYSLDDRWPFGELLCKLVHFLFYINLYGSILLLTCISVHQ 148
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YLVNLMVADLLYVLLPFLIITYSLDDRWPFGELLCKLVHFLFYINLYGSILLLTCISVHQ 120

Qy        149 FLGVCHPLCSLPYRTRRHAWLGTSTTWALVVLQLLPTLAFSHTDYINGQMIWYDMTSQEN 208
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FLGVCHPLCSLPYRTRRHAWLGTSTTWALVVLQLLPTLAFSHTDYINGQMIWYDMTSQEN 180

Qy        209 FDRLFAYGIVLTLSGFLSLLGHFGVLFTDGQEPDQARGEPHEDRQHSPSQVHPDHPTGVW 268
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FDRLFAYGIVLTLSGFLSLLGHFGVLFTDGQEPDQARGEPHEDRQHSPSQVHPDHPTGVW 240

Qy        269 PLHPLFCALPYHSLLLPHHLLSAFSGLPALDGSQCGLQDMEASGECEQ 316
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                     ||||||||||||||||||||||||||||||||||||||||||| :  |
Db        241 PLHPLFCALPYHSLLLPHHLLSAFSGLPALDGSQCGLQDMEASVKAMQ 288


RESULT 5
ADI16630
ID   ADI16630 standard; protein; 361 AA.
XX
AC   ADI16630;
XX
DT   15-APR-2004  (first entry)
XX
DE   Human NOVX protein to treat human pathological conditions SeqID166.
XX
KW   human; NOVX; cardiomyopathy; atherosclerosis; cancer; diabetes;
KW   inflammation; autoimmune disorder; allergy; blood disorder;
KW   acquired immunodeficiency syndrome; AIDS; obesity; asthma;
KW   immunoglobulin (Ig)A nephropathy; cirrhosis; arthritis;
KW   Alzheimer's disease; infection; stroke; muscular dystrophy; epilepsy;
KW   cytostatic; cardiant; antiinflammatory; immunosuppressive; antiallergic;
KW   haemostatic; anti-HIV; antidiabetic; antiarteriosclerotic; anorectic;
KW   antiasthmatic; nephrotropic; antiarthritic; hepatotropic;
KW   neuroprotective; nootropic; antibacterial; virucide; antiparasitic;
KW   relaxant; anticonvulsant; neurogenesis; wound healing; angiogenesis;
KW   chromosome mapping; tissue typing; pharmacogenomic; SNP;
KW   single nucleotide polymorphism.
XX
OS   Homo sapiens.
XX
PN   WO200268649-A2.
XX
PD   06-SEP-2002.
XX
PF   31-JAN-2002; 2002WO-US002785.
XX
PR   31-JAN-2001; 2001US-0265395P.
PR   31-JAN-2001; 2001US-0265412P.
PR   31-JAN-2001; 2001US-0265514P.
PR   31-JAN-2001; 2001US-0265517P.
PR   02-FEB-2001; 2001US-0266406P.
PR   05-FEB-2001; 2001US-0266767P.
PR   07-FEB-2001; 2001US-0266975P.
PR   07-FEB-2001; 2001US-0267057P.
PR   08-FEB-2001; 2001US-0267459P.
PR   09-FEB-2001; 2001US-0267823P.
PR   15-FEB-2001; 2001US-0268974P.
PR   26-FEB-2001; 2001US-0271664P.
PR   27-FEB-2001; 2001US-0271839P.
PR   27-FEB-2001; 2001US-0271855P.
PR   02-MAR-2001; 2001US-0272788P.
PR   02-MAR-2001; 2001US-0273046P.
PR   14-MAR-2001; 2001US-0275925P.
PR   14-MAR-2001; 2001US-0275947P.
PR   14-MAR-2001; 2001US-0275950P.
PR   14-MAR-2001; 2001US-0275989P.
PR   15-MAR-2001; 2001US-0276448P.
PR   15-MAR-2001; 2001US-0276450P.
PR   16-MAR-2001; 2001US-0276397P.
PR   16-MAR-2001; 2001US-0276768P.
PR   20-MAR-2001; 2001US-0278652P.
PR   26-MAR-2001; 2001US-0278775P.
PR   26-MAR-2001; 2001US-0278778P.
PR   29-MAR-2001; 2001US-0279882P.
PR   29-MAR-2001; 2001US-0279884P.
PR   30-MAR-2001; 2001US-0280147P.
PR   11-APR-2001; 2001US-0282992P.
PR   11-APR-2001; 2001US-0283083P.
PR   20-APR-2001; 2001US-0285133P.
PR   23-APR-2001; 2001US-0285749P.
PR   03-MAY-2001; 2001US-0288327P.
PR   03-MAY-2001; 2001US-0288504P.
PR   29-MAY-2001; 2001US-0294047P.
PR   30-MAY-2001; 2001US-0294473P.
PR   08-JUN-2001; 2001US-0296964P.
PR   18-JUN-2001; 2001US-0298959P.
PR   19-JUN-2001; 2001US-0299324P.
PR   13-AUG-2001; 2001US-0312020P.
PR   16-AUG-2001; 2001US-0312889P.
PR   16-AUG-2001; 2001US-0312908P.
PR   21-AUG-2001; 2001US-0313390P.
PR   28-AUG-2001; 2001US-0315470P.
PR   31-AUG-2001; 2001US-0316447P.
PR   07-SEP-2001; 2001US-0318115P.
PR   07-SEP-2001; 2001US-0318118P.
PR   12-SEP-2001; 2001US-0318740P.
PR   19-SEP-2001; 2001US-0323379P.
PR   18-OCT-2001; 2001US-0330245P.
PR   18-OCT-2001; 2001US-0330308P.
PR   14-NOV-2001; 2001US-0332701P.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Tchernev VT,  Spytek KA,  Zerhusen BD,  Patturajan M,  Shimkets RA;
PI   Li L,  Gangolli EA,  Padigaru M,  Anderson DW,  Rastelli L,  Miller CE;
PI   Gerlach VL,  Taupier RJ,  Gusev VY,  Colman SD,  Wolenc AR,  Pena CEA;
PI   Furtak K,  Grosse WM,  Alsobrook JP,  Lepley DM,  Rieger DK,  Burgess CE;
XX
DR   WPI; 2002-706998/76.
DR   N-PSDB; ADI16629.
XX
PT   New NOVX polypeptides and nucleic acids, useful for preventing or
PT   treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
PT   atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or
PT   pharmacogenomics.
XX
PS   Claim 1; SEQ ID NO 166; 1498pp; English.
XX
CC   This invention relates to a novel nucleic acids, and encoded polypeptides
CC   thereof, which have properties related to the stimulation of biochemical
CC   or physiological responses in a cell, tissue, organ or organism.
CC   Specifically, it refers to the use of biologically active fragments for
CC   diagnostic and prognostic assays and furthermore in the treatment of
CC   diverse pathological conditions. The present invention describes novel
CC   human and murine NOVX proteins, as well as methods to modulate their
CC   expression using antisense oligos, ribozymes and peptide nucleic acids.
CC   The NOVX polypeptides, polynucleotides and antibodies are useful in
CC   treating or preventing NOVX-associated disorders, e.g. cardiomyopathy,
CC   atherosclerosis, cancer and diabetes. Furthermore, they may be used in
CC   treating or preventing diseases such as inflammation, autoimmune
CC   disorders, allergies, blood disorders, acquired immunodeficiency syndrome
CC   (AIDS), obesity, asthma, immunoglobulin (Ig)A nephropathy, cirrhosis,
CC   arthritis, Alzheimer's disease, infections, stroke, muscular dystrophy
CC   and epilepsy. Accordingly, these molecules have many activities including
CC   cytostatic, cardiant, antiinflammatory, immunosuppressive, antiallergic,
CC   haemostatic, anti-HIV, antidiabetic, antiarteriosclerotic, anorectic,
CC   antiasthmatic, nephrotropic, antiarthritic, hepatotropic,
CC   neuroprotective, nootropic, antibacterial, virucide, antiparasitic,
CC   relaxant and anticonvulsant. In addition, they are useful in screening
CC   assays to identify small molecules that modulate or inhibit, for example,
CC   neurogenesis, wound healing and angiogenesis. The nucleic acids are also
CC   used as in chromosome mapping, tissue typing, preventive medicine and
CC   pharmacogenomics. This polypeptide is a human NOVX protein of the
CC   invention.
XX
SQ   Sequence 361 AA;

  Query Match             79.0%;  Score 1529;  DB 5;  Length 361;
  Best Local Similarity   82.6%;  Pred. No. 1.5e-161;
  Matches  303;  Conservative   11;  Mismatches   39;  Indels   14;  Gaps    5;

Qy          1 MLSILLPSRGSRSGSRRGALLLEGASRDMEKVDMNTSQEQGLCQFSEKYKQVYLSLAYSI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLSILLPSRGSRSGSRRGALLLEGASRDMEKVDMNTSQEQGLCQFSEKYKQVYLSLAYSI 60

Qy         61 IFILGLPLNGTVLWHSWGQTKRWSCATTYLVNLMVADLLLYVLLPFLIITYSLDDRWPFGE 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db         61 IFILGLPLNGTVLWHSWGQTKRWSCATTYLVNLMVADLLYVLLPFLIITYSLDDRWPFGE 120

Qy        121 LLCKLVHFLFYINLYGSILLLTCISVHQFLGVCHPLCSLPYRTRRHAWLGTSTTWALVVL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLCKLVHFLFYINLYGSILLLTCISVHQFLGVCHPLCSLPYRTRRHAWLGTSTTWALVVL 180

Qy        181 QLLPTLAFSHTDYINGQMIWYDMTSQENFDRLFAYGIVLTLSGFLSLLGHFGVLFTDGQE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 QLLPTLAFSHTDYINGQMIWYDMTSQENFDRLFAYGIVLTLSGFLSLLGHFGVYSL---- 236

Qy        241 PDQARG--EPHEDRQHSPSQVHPDHPTGVWPLHPLF--CALPYHSLLLPHHLLSAF---S 293
                  :| |:    : :        :  :   ||  | :|:| :     :|    |
Db        237 --MVRSLIKPEENLMRTGNTARARSIRTILLVCGLFTLCFVPFH-ITRSFYLTICFLLSQ 293

Qy        294 GLPALDGSQCGLQDMEASGECEQLPQPSPVLSFKGGKNRVRLLQKLRQNKLGEHPAGRKR 353
                |  :||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        294 DCQLLMAAQCGLQDMEASGECEQLPQPSPVLSFKGGKNRVRLLQKLRQNKLGEHPAGRKR 353

Qy        354 CPGLNRS 360
              |||||||
Db        354 CPGLNRS 360
```

RESULT 6
ADN42284
ID ADN42284 standard; protein; 361 AA.
XX
AC ADN42284;
XX
DT 17-JUN-2004 (first entry)
XX
DE Human novel proteinNOV 43.
XX
KW Human; NOVX; cancer; diabetes; cardiomyopathy; atherosclerosis; SNP;
KW single nucleotide polymorphism.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 162
FT /note= "May be Pro as the result of a single nucleotide
FT polymorphism"
XX
PN US2004033493-A1.
XX
PD 19-FEB-2004.
XX
PF 31-JAN-2002; 2002US-00072012.
XX
PR 31-JAN-2001; 2001US-0265395P.
PR 31-JAN-2001; 2001US-0265412P.
PR 31-JAN-2001; 2001US-0265514P.
PR 31-JAN-2001; 2001US-0265517P.
PR 02-FEB-2001; 2001US-0266406P.
PR 05-FEB-2001; 2001US-0266767P.
PR 07-FEB-2001; 2001US-0266975P.
PR 07-FEB-2001; 2001US-0267057P.
PR 08-FEB-2001; 2001US-0267459P.
PR 09-FEB-2001; 2001US-0267823P.
PR 15-FEB-2001; 2001US-0268974P.
PR 26-FEB-2001; 2001US-0271664P.
PR 27-FEB-2001; 2001US-0271839P.
PR 27-FEB-2001; 2001US-0271855P.
PR 02-MAR-2001; 2001US-0272788P.
PR 02-MAR-2001; 2001US-0273046P.
PR 14-MAR-2001; 2001US-0275925P.
PR 14-MAR-2001; 2001US-0275947P.
PR 14-MAR-2001; 2001US-0275950P.
PR 14-MAR-2001; 2001US-0275989P.
PR 15-MAR-2001; 2001US-0276448P.
PR 15-MAR-2001; 2001US-0276450P.
PR 16-MAR-2001; 2001US-0276397P.
PR 16-MAR-2001; 2001US-0276768P.
PR 20-MAR-2001; 2001US-0278652P.
PR 26-MAR-2001; 2001US-0278775P.
PR 26-MAR-2001; 2001US-0278778P.
PR 29-MAR-2001; 2001US-0279882P.
PR 29-MAR-2001; 2001US-0279884P.
PR 30-MAR-2001; 2001US-0280147P.
PR 11-APR-2001; 2001US-0282992P.
PR 11-APR-2001; 2001US-0283083P.
PR 20-APR-2001; 2001US-0285133P.
PR 23-APR-2001; 2001US-0285749P.
PR 03-MAY-2001; 2001US-0288327P.
PR 03-MAY-2001; 2001US-0288504P.
PR 29-MAY-2001; 2001US-0294047P.
PR 30-MAY-2001; 2001US-0294473P.
PR 08-JUN-2001; 2001US-0296964P.
PR 18-JUN-2001; 2001US-0298959P.
PR 19-JUN-2001; 2001US-0299324P.
PR 13-AUG-2001; 2001US-0312020P.
PR 16-AUG-2001; 2001US-0312889P.
PR 16-AUG-2001; 2001US-0312908P.
PR 21-AUG-2001; 2001US-0313930P.
PR 28-AUG-2001; 2001US-0315470P.
PR 31-AUG-2001; 2001US-0316447P.
PR 07-SEP-2001; 2001US-0318115P.
PR 07-SEP-2001; 2001US-0318118P.
PR 12-SEP-2001; 2001US-0318740P.
PR 19-SEP-2001; 2001US-0323379P.
PR 18-OCT-2001; 2001US-0330245P.
PR 18-OCT-2001; 2001US-0330308P.
PR 14-NOV-2001; 2001US-0332701P.
XX
PA (TCHE/) TCHERNEV V T.
PA (SPYT/) SPYTEK K A.
PA (ZERH/) ZERHUSEN B D.
PA (PATT/) PATTURAJAN M.
PA (SHIM/) SHIMKETS R A.
PA (LILL/) LI L.
PA (GANG/) GANGOLLI E A.
PA (PADI/) PADIGARU M.
PA (ANDE/) ANDERSON D W.
PA (RAST/) RASTELLI L.
PA (MILL/) MILLER C E.
PA (GERL/) GERLACH V.
PA (TAUP/) TAUPIER R J.
PA (GUSE/) GUSEV V Y.
PA (COLM/) COLMAN S D.
PA (WOLE/) WOLENC A R.
PA (PENA/) PENA C E A.
PA (FURT/) FURTAK K.
PA (GROS/) GROSSE W M.
PA (ALSO/) ALSOBROOK J P.
PA (LEPL/) LEPLEY D M.
PA (RIEG/) RIEGER D K.
PA (BURG/) BURGESS C E.
XX
PI Tchernev VT, Spytek KA, Zerhusen BD, Patturajan M, Shimkets RA;
PI Li L, Gangolli EA, Padigaru M, Anderson DW, Rastelli L, Miller CE;
PI Gerlach V, Taupier RJ, Gusev VY, Colman SD, Wolenc AR, Pena CEA;
PI Furtak K, Grosse WM, Alsobrook JP, Lepley DM, Rieger DK, Burgess CE;
XX
DR WPI; 2004-180039/17.
DR N-PSDB; ADN42283.
XX
PT Isolated NOVX polypeptides and polynucleotides, useful for preventing
PT diagnosing and/or treating cancer, diabetes, cardiomyopathy and
PT atherosclerosis.
XX
PS Claim 1; SEQ ID NO 166; 1309pp; English.
XX
CC The invention relates isolated 162 NOVX polypeptides (NOV1-NOV99,
CC including splice variants) and the nucleic acids (NA) that encode them.
CC Also included are the mature NOVX proteins (and their encoding
CC polynucleotides), a vector comprising NOVX NA, a cell comprising the

```
CC   vector, an antibody that binds immunospecifically to NOVX, determining
CC   the presence or amount of NOVX in a sample, determining the presence or
CC   amount of NOVX NA in a sample, identifying an agent that binds to NOVX,
CC   modulating the activity of NOVX, treating or preventing a NOVX-associated
CC   disorder, determining the presence of or predisposition to a disease
CC   associated with altered levels of NOVX and treating a pathological state
CC   in a mammal comprising administering a polypeptide which is at least 95%
CC   identical to NOVX (or fragment). NOVX and NA may be used in the
CC   prevention, treatment and diagnosis of diseases associated with
CC   inappropriate expression and activity of NOVX (e.g. cancer, diabetes,
CC   cardiomyopathy and/or atherosclerosis). The anti-NOVX antibodies and
CC   antagonists may also be used to down regulate expression and activity of
CC   NOVX. The anti-NOVX antibodies may also be used as diagnostic agents for
CC   detecting the presence of NOVX in samples (e.g. by enzyme linked
CC   immunosorbant assay (ELISA). The agents and methods may be used in this
CC   way to prevent, diagnose and treat cancer, diabetes, cardiomyopathy
CC   and/or atherosclerosis. The present sequence represents a NOVX protein.
XX
SQ   Sequence 361 AA;

  Query Match             78.5%;  Score 1519;  DB 8;  Length 361;
  Best Local Similarity   82.3%;  Pred. No. 2e-160;
  Matches  302;  Conservative   11;  Mismatches   40;  Indels   14;  Gaps    5;

Qy          1 MLSILLPSRGSRSGSRRGALLLEGASRDMEKVDMNTSQEQGLCQFSEKYKQVYLSLAYSI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLSILLPSRGSRSGSRRGALLLEGASRDMEKVDMNTSQEQGLCQFSEKYKQVYLSLAYSI 60

Qy         61 IFILGLPLNGTVLWHSWGQTKRWSCATTYLVNLMVADLLYVLLPFLIITYSLDDRWPFGE 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 IFILGLPLNGTVLWHSWGQTKRWSCATTYLVNLMVADLLYVLLPFLIITYSLDDRWPFGE 120

Qy        121 LLCKLVHFLFYINLYGSILLLTCISVHQFLGVCHPLCSLPYRTRRHAWLGTSTTWALVVL 180
              |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        121 LLCKLVHFLFYINLYGSILLLTCISVHQFLGVSHPLCSLPYRTRRHAWLGTSTTWALVVL 180

Qy        181 QLLPTLAFSHTDYINGQMIWYDMTSQENFDRLFAYGIVLTLSGFLSLLGHFGVLFTDGQE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 QLLPTLAFSHTDYINGQMIWYDMTSQENFDRLFAYGIVLTLSGFLSLLGHFGVYSL---- 236

Qy        241 PDQARG--EPHEDRQHSPSQVHPDHPTGVWPLHPLF--CALPYHSLLLPHHLLSAF---S 293
                  |   :| |:   : :         :  :  ||  | :|:| :    :|   |
Db        237 --MVRSLIKPEENLMRTGNTARARSIRTILLVCGLFTLCFVPFH-ITRSFYLTICFLLSQ 293

Qy        294 GLPALDGSQCGLQDMEASGECEQLPQPSPVLSFKGGKNRVRLLQKLRQNKLGEHPAGRKR 353
                | :||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        294 DCQLLMAAQCGLQDMEASGECEQLPQPSPVLSFKGGKNRVRLLQKLRQNKLGEHPAGRKR 353

Qy        354 CPGLNRS 360
              |||||||
Db        354 CPGLNRS 360


RESULT 7
ADC26009
ID   ADC26009 standard; protein; 338 AA.
XX
AC   ADC26009;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Human purinergic receptor P2Y-related GPCRx6 alternative protein.
XX
KW   virucide; fungicide; antibacterialc; cytostatic; analgesic; antidiabetic;
KW   anorectic; cardiant; hypotensive; osteopathic; antianginal;
KW   antiarteriosclerotic; cerebroprotective; anti-ulcer; antiallergic;
KW   nootropic; neuroprotective; antiparkinsonian; G-protein coupled receptor;
KW   GPCR; viral; fungal; bacterial infection; immune-related disorder;
KW   cancer; pain; diabetes; obesity; anorexia; acute heart failure;
KW   hypertension; osteoporosis; angina pectoris; atherosclerosis; stroke;
KW   ulcer; allergy; psychotic neurological disorder; schizophrenia; dementia;
KW   degenerative disease; Parkinson's; Alzheimer's; dyskinesia; Huntington's;
KW   human; GPCRx6; purinergic receptor P2Y.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 270
FT                   /note= "Encoded by TTC"
XX
PN   US2003088080-A1.
XX
PD   08-MAY-2003.
XX
PF   21-JUN-2001; 2001US-00885453.
XX
PR   20-JUN-2000; 2000US-0212908P.
PR   05-DEC-2000; 2000EP-00870289.
XX
PA   (COMM/) COMMUNI D.
PA   (LANN/) LANNOY V.
PA   (GOVA/) GOVAERTS C.
PA   (PARM/) PARMENTIER M.
PA   (DETH/) DETHEUX M.
XX
PI   Communi D,  Lannoy V,  Govaerts C,  Parmentier M,  Detheux M;
XX
DR   WPI; 2003-657983/62.
DR   N-PSDB; ADC25999.
XX
PT   New human G-protein coupled receptor, useful for treating receptor-
PT   mediated disorders, e.g. infections, cancer, pain, diabetes, obesity,
PT   acute heart failure, osteoporosis, stroke, ulcer, allergy, or
PT   neurological disorders.
XX
PS   Example 3; Page 15; 24pp; English.
XX
CC   The invention relates to a novel G-protein coupled receptor (GPCR). The
CC   receptor, polynucleotide, agonist, reverse agonist and antagonist of the
CC   invention may be useful for treating receptor-mediated disorders
CC   including viral, fungal or bacterial infections, immune-related disorders
CC   such as cancer, pain, diabetes, obesity, anorexia, acute heart failure,
CC   hypertension, osteoporosis, angina pectoris, atherosclerosis, stroke,
CC   ulcer and allergy, as well as psychotic and neurological disorders such
CC   as schizophrenia and dementia, degenerative diseases such as Parkinson's
CC   disease and Alzheimer's disease and dyskinesias such as Huntington's
CC   disease. The current sequence is that of the human purinergic receptor
CC   P2Y-related GPCRx6 alternative protein of the invention.
XX
SQ   Sequence 338 AA;

  Query Match             61.4%;  Score 1189;  DB 7;  Length 338;
  Best Local Similarity   98.7%;  Pred. No. 1.3e-123;
  Matches  225;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 MLSILLPSRGSRSGSRRGALLLEGASRDMEKVDMNTSQEQGLCQFSEKYKQVYLSLAYSI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLSILLPSRGSRSGSRRGALLLEGASRDMEKVDMNTSQEQGLCQFSEKYKQVYLSLAYSI 60

Qy         61 IFILGLPLNGTVLWHSWGQTKRWSCATTYLVNLMVADLLYVLLPFLIITYSLDDRWPFGE 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 IFILGLPLNGTVLWHSWGQTKRWSCATTYLVNLMVADLLYVLLPFLIITYSLDDRWPFGE 120

Qy        121 LLCKLVHFLFYINLYGSILLLTCISVHQFLGVCHPLCSLPYRTRRHAWLGTSTTWALVVL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLCKLVHFLFYINLYGSILLLTCISVHQFLGVCHPLCSLPYRTRRHAWLGTSTTWALVVL 180

Qy        181 QLLPTLAFSHTDYINGQMIWYDMTSQENFDRLFAYGIVLTLSGFLSLL 228
              |||||||||||||||||||||||||||||||||||||||||||||||   |
Db        181 QLLPTLAFSHTDYINGQMIWYDMTSQENFDRLFAYGIVLTLSGFFPSL 228


RESULT 8
ABW00804
ID   ABW00804 standard; protein; 338 AA.
XX
```

```
AC   ABW00804;
XX
DT   15-JAN-2004  (first entry)
XX
DE   Human GPCRx6 protein.
XX
KW   Human; G-protein coupled receptor; GPCR; infection; neoplastic process;
KW   inflammation; myocardial infarction; atherosclerosis; angina pectoris;
KW   hypertension; osteoporosis; antibacterial; cytostatic; fungicide; pain;
KW   diabetes; cancer; virucide; analgesic; cardiant.
XX
OS   Homo sapiens.
XX
PN   US2003108986-A1.
XX
PD   12-JUN-2003.
XX
PF   20-FEB-2002; 2002US-00079384.
XX
PR   21-JUN-2001; 2001US-00885453.
XX
PA   (EURO-) EUROSCREEN SA.
XX
PI   Communi D,  Lannoy V,  Brezillon S,  Detheux M,  Parmentier M;
PI   Govaerts C;
XX
DR   WPI; 2003-810852/76.
DR   N-PSDB; AAD61648.
XX
PT   Novel G-protein coupled receptor useful for treating viral infections,
PT   bacterial infections, fungal infections, cancer, diabetes, hypertension,
PT   osteoporosis, angina pectoris, myocardial infarction, atherosclerosis.
XX
PS   Claim 1; Fig 4; 0pp; English.
XX
CC   The present invention relates to novel G-protein coupled receptors
CC   (GPCRs) and the nucleic acids encoding them. The invention is useful for
CC   treating viral, bacterial and fungal infections, inflammatory and
CC   neoplastic processes, pain, diabetes, hypertension, osteoporosis, cancer,
CC   angina pectoris, myocardial infarction and atherosclerosis. The present
CC   sequence is human G-protein coupled receptor (GPCR) protein
XX
SQ   Sequence 338 AA;

  Query Match             61.4%;  Score 1189;  DB 7;  Length 338;
  Best Local Similarity   98.7%;  Pred. No. 1.3e-123;
  Matches  225;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 MLSILLPSRGSRSGSRRGALLLEGASRDMEKVDMNTSQEQGLCQFSEKYKQVYLSLAYSI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLSILLPSRGSRSGSRRGALLLEGASRDMEKVDMNTSQEQGLCQFSEKYKQVYLSLAYSI 60

Qy         61 IFILGLPLNGTVLWHSWGQTKRWSCATTYLVNLMVADLLYVLLPFLIITYSLDDRWPFGE 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 IFILGLPLNGTVLWHSWGQTKRWSCATTYLVNLMVADLLYVLLPFLIITYSLDDRWPFGE 120

Qy        121 LLCKLVHFLFYINLYGSILLLTCISVHQFLGVCHPLCSLPYRTRRHAWLGTSTTWALVVL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLCKLVHFLFYINLYGSILLLTCISVHQFLGVCHPLCSLPYRTRRHAWLGTSTTWALVVL 180

Qy        181 QLLPTLAFSHTDYINGQMIWYDMTSQENFDRLFAYGIVLTLSGFLSLL 228
              |||||||||||||||||||||||||||||||||||||||||||||||    |
Db        181 QLLPTLAFSHTDYINGQMIWYDMTSQENFDRLFAYGIVLTLSGFFPSL 228


RESULT 9
ABB98146
ID   ABB98146 standard; protein; 339 AA.
XX
AC   ABB98146;
XX
DT   17-OCT-2002  (first entry)
XX
DE   Human GPCR designated PFI-020'.
XX
KW   Human; GPCR; G-protein coupled receptor; antidepressant; neuroleptic;
KW   gene therapy; therapeutic; mood; depression; arousal; eating; sleeping;
KW   disorder; PFI-020'.
XX
OS   Homo sapiens.
XX
PN   EP1215214-A1.
XX
PD   19-JUN-2002.
XX
PF   04-DEC-2001; 2001EP-00310137.
XX
PR   18-DEC-2000; 2000GB-00030855.
PR   17-JAN-2001; 2001GB-00001222.
XX
PA   (PFIZ ) PFIZER LTD.
PA   (PFIZ ) PFIZER INC.
XX
PI   Fidock MD;
XX
DR   WPI; 2002-510798/55.
DR   N-PSDB; ABQ79300.
XX
PT   New polynucleotide encoding G protein-coupled receptor PFI-020, useful
PT   e.g. for treating eating and sleeping disorders and for identifying
PT   specific modulators.
XX
PS   Claim 1 (b); Page 13; 23pp; English.
XX
CC   The invention relates to an isolated polynucleotide encoding a novel
CC   polypeptide belonging to the class of proteins known as G-protein coupled
CC   receptors (GPCRs). The activity of proteins of the invention may be
CC   described as, antidepressant and neuroleptic. Polynucleotides of the
CC   invention are used for recombinant expression of the G protein-coupled
CC   receptor (PFI-020) polypeptides, to create transgenic animals, as source
CC   of primers, probes, antisense sequences and ribozymes and in gene
CC   therapy. Therapeutic agents of the invention can be used to treat a wide
CC   range of disorders, particularly mood disorders, depression or arousal,
CC   especially eating and sleeping disorders. The current sequence represents
CC   a human GPCR designated PFI-020'
XX
SQ   Sequence 339 AA;

  Query Match             61.2%;  Score 1185;  DB 5;  Length 339;
  Best Local Similarity   99.6%;  Pred. No. 3.7e-123;
  Matches  225;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MLSILLPSRGSRSGSRRGALLLEGASRDMEKVDMNTSQEQGLCQFSEKYKQVYLSLAYSI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLSILLPSRGSRSGSRRGALLLEGASRDMEKVDMNTSQEQGLCQFSEKYKQVYLSLAYSI 60

Qy         61 IFILGLPLNGTVLWHSWGQTKRWSCATTYLVNLMVADLLYVLLPFLIITYSLDDRWPFGE 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 IFILGLPLNGTVLWHSWGQTKRWSCATTYLVNLMVADLLYVLLPFLIITYSLDDRWPFGE 120

Qy        121 LLCKLVHFLFYINLYGSILLLTCISVHQFLGVCHPLCSLPYRTRRHAWLGTSTTWALVVL 180
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        121 LLCKLVHFLFYINLYGSILLLTCISVHQFLGVWHPLCSLPYRTRRHAWLGTSTTWALVVL 180

Qy        181 QLLPTLAFSHTDYINGQMIWYDMTSQENFDRLFAYGIVLTLSGFLS 226
              |||||||||||||||||||||||||||||||||||||||||||||||
Db        181 QLLPTLAFSHTDYINGQMIWYDMTSQENFDRLFAYGIVLTLSGFLS 226


RESULT 10
AAE18640
ID   AAE18640 standard; protein; 339 AA.
XX
AC   AAE18640;
XX
DT   17-MAY-2002  (first entry)
```

XX
DE Human G-protein coupled receptor (GCREC-1).
XX
KW Human; G-protein coupled receptor; GCREC-1; cell proliferative disorder;
KW neurological; cardiovascular; gastrointestinal; autoimmune; inflammatory;
KW metabolic; hepatitis; psoriasis; cancer; epilepsy; Alzheimer's disease;
KW Pick's disease; Huntington's disease; Parkinson's disease; hypertension;
KW atherosclerosis; myocardial infarction; gastritis; cirrhosis; cytostatic;
KW osteoporosis; Crohn's disease; acquired immunodeficiency syndrome; AIDS;
KW anaemia; asthma; rheumatoid arthritis; diabetes; obesity; drug screening;
KW transgenic animal; allergy; gene therapy; hepatotropic; anticonvulsant;
KW nootropic; neuroprotective; cardiant; immunosuppressive; anorectic;
KW virucide; receptor.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 89. .109
FT /note= "Transmembrane domain"
FT Domain 130. .149
FT /note= "Transmembrane domain"
XX
PN WO200210387-A2.
XX
PD 07-FEB-2002.
XX
PF 25-JUL-2001; 2001WO-US023433.
XX
PR 27-JUL-2000; 2000US-0221478P.
PR 03-AUG-2000; 2000US-0223268P.
PR 21-AUG-2000; 2000US-0227054P.
PR 08-SEP-2000; 2000US-0231121P.
PR 13-SEP-2000; 2000US-0232243P.
PR 15-SEP-2000; 2000US-0232691P.
PR 22-SEP-2000; 2000US-0235146P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Thornton M, Patterson C, Lal P, Burford N, Yue H, Gandhi AR;
PI Elliot VS, Ramkumar J, Baughn MR, Kallick DA, Walia NK, Hafalia AJA;
PI Yao MG, Lu Y, Tribouley CM, Policky JL, Kearney L, Graul RC;
PI Warren BA, Lee EA, Ding L;
XX
DR WPI; 2002-188744/24.
DR N-PSDB; AAD29667.
XX
PT New human G-protein coupled receptor polypeptide for diagnosis,
PT prevention and treatment of cell proliferative, neurological,
PT cardiovascular, gastrointestinal, autoimmune/inflammatory, and metabolic
PT disorders.
XX
PS Claim 1; Page 114-115; 150pp; English.
XX
CC The invention relates to novel human G-protein coupled receptors (GCREC)
CC and their encoding polynucleotides. GCREC is useful as an immunogen for
CC preparing monoclonal and polyclonal antibodies. GCREC is useful for
CC diagnosing, treating and preventing a cell proliferative disorder (e.g.,
CC hepatitis, psoriasis, cancer), a neurological disorder (e.g., epilepsy,
CC Alzheimer's disease, Pick's disease, Huntington's disease, Parkinson's
CC disease), a cardiovascular disorder (e.g., atherosclerosis, hypertension,
CC myocardial infarction), gastrointestinal disorder (e.g., gastritis,
CC cirrhosis, Crohn's disease), an autoimmune/ inflammatory disorder (e.g.,
CC acquired immunodeficiency syndrome (AIDS), allergy, anaemia, asthma,
CC rheumatoid arthritis), a metabolic disorder (e.g., diabetes, obesity,
CC osteoporosis), and viral infections. GCREC is useful in a number of drug
CC screening techniques, and to analyse the proteome of a tissue or cell
CC type. GCREC is useful for creating knockin humanised animals or
CC transgenic animals to model human diseases, in somatic or germline gene
CC therapy, to generate a transcript image of a tissue or cell type, for
CC detecting differences in the chromosomal location due to translocation,
CC inversion, etc., among normal, carrier or affected individuals, and as
CC hybridization probes for mapping naturally occurring genomic sequences.
CC GCREC is useful in Southern or northern analysis, dot blot or other
CC membrane-based technologies, in PCR technologies, in dipstick, pin,
CC multiformat enzyme linked immunosorbant (ELISA)-like assays, and in
CC microarrays utilising fluids or tissues from patients to detect altered
CC GCREC expression. The present sequence is human GCREC-1
XX
SQ Sequence 339 AA;

Query Match 61.2%; Score 1185; DB 5; Length 339;
Best Local Similarity 99.6%; Pred. No. 3.7e-123;
Matches 225; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 MLSILLPSRGSRSGSRRGALLLEGASRDMEKVDMNTSQEQGLCQFSEKYKQVYLSLAYSI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLSILLPSRGSRSGSRRGALLLEGASRDMEKVDMNTSQEQGLCQFSEKYKQVYLSLAYSI 60

Qy         61 IFILGLPLNGTVLWHSWGQTKRWSCATTYLVNLMVADLLYVLLPFLIITYSLDDRWPFGE 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 IFILGLPLNGTVLWHSWGQTKRWSCATTYLVNLMVADLLYVLLPFLIITYSLDDRWPFGE 120

Qy        121 LLCKLVHFLFYINLYGSILLLTCISVHQFLGVCHPLCSLPYRTRRHAWLGTSTTWALVVL 180
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        121 LLCKLVHFLFYINLYGSILLLTCISVHQFLGVWHPLCSLPYRTRRHAWLGTSTTWALVVL 180

Qy        181 QLLPTLAFSHTDYINGQMIWYDMTSQENFDRLFAYGIVLTLSGFLS 226
              |||||||||||||||||||||||||||||||||||||||||||||
Db        181 QLLPTLAFSHTDYINGQMIWYDMTSQENFDRLFAYGIVLTLSGFLS 226
```

RESULT 11
ADO30394
ID ADO30394 standard; protein; 339 AA.
XX
AC ADO30394;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human GPCR P2Y3L, SEQ ID NO:1497.
XX
KW G protein-coupled receptor; GPCR; drug screening; diagnosis;
KW transgenic mouse; neurological disorder; adrenal gland disorder;
KW colon disorder; intestinal disorder; cardiovascular disorder;
KW muscular disorder; blood disorder; immune disorder; bone disorder;
KW joint disorder; metabolic disorder; nutritive disorder; cancer;
KW kidney disorder; liver disorder; lung disorder; breast disorder;
KW ovary disorder; uterus disorder; prostate disorder; testis disorder;
KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;
KW thymus disorder; thyroid disorder; antiparkinsonian; antimanic;
KW cytostatic; antiinflammatory; vasotropic; antianginal; antiarrhythmic;
KW CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;
KW virucide; hepatotropic; antibacterial; antianaemic; antiseborrhoeic;
KW dermatological; antiulcer; antithyroid; antiallergic; anorectic;
KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;
KW receptor.
XX
OS Homo sapiens.
XX
PN WO2004040000-A2.
XX
PD 13-MAY-2004.
XX
PF 09-SEP-2003; 2003WO-US028226.
XX
PR 09-SEP-2002; 2002US-0409303P.
PR 09-APR-2003; 2003US-0461329P.
XX
PA (PRIM-) PRIMAL INC.
XX
PI Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;
PI Madisen L, Mcilwain KL, Pavlova MN, Vassilatis D, Zeng H;
XX
DR WPI; 2004-390329/36.
DR N-PSDB; ADO30395.
XX

```
PT   Novel mammalian G protein coupled receptors, useful for identifying
PT   compounds that modulates diagnosing and treating disease condition
PT   associated with GPCR dysfunction e.g. autoimmune diseases, angina
PT   pectoris, Parkinson's disease.
XX
PS   Claim 151; SEQ ID NO 1497; 542pp; English.
XX
CC   The invention relates to human and mouse G protein-coupled receptors
CC   (GPCRs) and nucleic acids encoding them. The invention also relates to
CC   sequences at least 90% identical to the GPCR proteins and nucleic acids
CC   of the invention; methods of treating, preventing or diagnosing diseases
CC   associated with GPCRs of the invention; methods of screening for
CC   compounds useful in the treatment of GPCR-related diseases; a transgenic
CC   mouse comprising a GPCR gene of the invention; a mouse comprising a
CC   mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived
CC   from the trasngenic mice; kits comprising several mice, each of which has
CC   a mutation in a different GPCR gene of the invention; and kits comprising
CC   probes which hybridise to GPCR polynucleotides of the invention. The
CC   invention further discloses variants of the GPCR polypeptides and vectors
CC   comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
CC   be used in the diagnosis, treatment or prevention of a wide variety of
CC   diseases including neurological disorders (e.g., Alzheimer's disease,
CC   depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
CC   disorders of the adrenal gland; disorders of the colon or intestine
CC   (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel
CC   syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
CC   myocardial infarction); muscular disorders; blood disorders (e.g.,
CC   anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or
CC   AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid
CC   arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
CC   obesity, enzyme deficiency-related diseases or vitamin deficiency-related
CC   diseases); and disorders of the kidney, liver, lung, breast, ovary,
CC   uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
CC   thyroid (e.g., cancers). The present sequence represents a GPCR of the
CC   invention. Note: The full sequence data for this patent did not form part
CC   of the printed specification; those sequences not shown were obtained in
CC   electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 339 AA;

  Query Match             61.2%;  Score 1185;  DB 8;  Length 339;
  Best Local Similarity   99.6%;  Pred. No. 3.7e-123;
  Matches  225;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MLSILLPSRGSRSGSRRGALLLEGASRDMEKVDMNTSQEQGLCQFSEKYKQVYLSLAYSI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLSILLPSRGSRSGSRRGALLLEGASRDMEKVDMNTSQEQGLCQFSEKYKQVYLSLAYSI 60

Qy         61 IFILGLPLNGTVLWHSWGQTKRWSCATTYLVNLMVADLLYVLLPFLIITYSLDDRWPFGE 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 IFILGLPLNGTVLWHSWGQTKRWSCATTYLVNLMVADLLYVLLPFLIITYSLDDRWPFGE 120

Qy        121 LLCKLVHFLFYINLYGSILLLTCISVHQFLGVCHPLCSLPYRTRRHAWLGTSTTWALVVL 180
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        121 LLCKLVHFLFYINLYGSILLLTCISVHQFLGVWHPLCSLPYRTRRHAWLGTSTTWALVVL 180

Qy        181 QLLPTLAFSHTDYINGQMIWYDMTSQENFDRLFAYGIVLTLSGFLS 226
              |||||||||||||||||||||||||||||||||||||||||||||
Db        181 QLLPTLAFSHTDYINGQMIWYDMTSQENFDRLFAYGIVLTLSGFLS 226


RESULT 12
ADC26000
ID   ADC26000 standard; protein; 338 AA.
XX
AC   ADC26000;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Human purinergic receptor P2Y-related GPCRx6 protein.
XX
KW   virucide; fungicide; antibacterialc; cytostatic; analgesic; antidiabetic;
KW   anorectic; cardiant; hypotensive; osteopathic; antianginal;
KW   antiarteriosclerotic; cerebroprotective; anti-ulcer; antiallergic;
KW   nootropic; neuroprotective; antiparkinsonian; G-protein coupled receptor;
KW   GPCR; viral; fungal; bacterial infection; immune-related disorder;
KW   cancer; pain; diabetes; obesity; anorexia; acute heart failure;
KW   hypertension; osteoporosis; angina pectoris; atherosclerosis; stroke;
KW   ulcer; allergy; psychotic neurological disorder; schizophrenia; dementia;
KW   degenerative disease; Parkinson's; Alzheimer's; dyskinesia; Huntington's;
KW   human; GPCRx6; purinergic receptor P2Y.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 62
FT                   /note= "Encoded by TTT"
FT   Misc-difference 243
FT                   /note= "Encoded by AAG"
XX
PN   US2003088080-A1.
XX
PD   08-MAY-2003.
XX
PF   21-JUN-2001; 2001US-00885453.
XX
PR   20-JUN-2000; 2000US-0212908P.
PR   05-DEC-2000; 2000EP-00870289.
XX
PA   (COMM/) COMMUNI D.
PA   (LANN/) LANNOY V.
PA   (GOVA/) GOVAERTS C.
PA   (PARM/) PARMENTIER M.
PA   (DETH/) DETHEUX M.
XX
PI   Communi D,  Lannoy V,  Govaerts C,  Parmentier M,  Detheux M;
XX
DR   WPI; 2003-657983/62.
DR   N-PSDB; ADC25999.
XX
PT   New human G-protein coupled receptor, useful for treating receptor-
PT   mediated disorders, e.g. infections, cancer, pain, diabetes, obesity,
PT   acute heart failure, osteoporosis, stroke, ulcer, allergy, or
PT   neurological disorders.
XX
PS   Example 3; Page 15-16; 24pp; English.
XX
CC   The invention relates to a novel G-protein coupled receptor (GPCR). The
CC   receptor, polynucleotide, agonist, reverse agonist and antagonist of the
CC   invention may be useful for treating receptor-mediated disorders
CC   including viral, fungal or bacterial infections, immune-related disorders
CC   such as cancer, pain, diabetes, obesity, anorexia, acute heart failure,
CC   hypertension, osteoporosis, angina pectoris, atherosclerosis, stroke,
CC   ulcer and allergy, as well as psychotic and neurological disorders such
CC   as schizophrenia and dementia, degenerative diseases such as Parkinson's
CC   disease and Alzheimer's disease and dyskinesias such as Huntington's
CC   disease. The current sequence is that of the human purinergic receptor
CC   P2Y-related GPCRx6 protein of the invention.
XX
SQ   Sequence 338 AA;

  Query Match             60.9%;  Score 1179;  DB 7;  Length 338;
  Best Local Similarity   98.2%;  Pred. No. 1.7e-122;
  Matches  224;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 MLSILLPSRGSRSGSRRGALLLEGASRDMEKVDMNTSQEQGLCQFSEKYKQVYLSLAYSI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLSILLPSRGSRSGSRRGALLLEGASRDMEKVDMNTSQEQGLCQFSEKYKQVYLSLAYSI 60

Qy         61 IFILGLPLNGTVLWHSWGQTKRWSCATTYLVNLMVADLLYVLLPFLIITYSLDDRWPFGE 120
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 IPILGLPLNGTVLWHSWGQTKRWSCATTYLVNLMVADLLYVLLPFLIITYSLDDRWPFGE 120

Qy        121 LLCKLVHFLFYINLYGSILLLTCISVHQFLGVCHPLCSLPYRTRRHAWLGTSTTWALVVL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        121 LLCKLVHFLFYINLYGSILLLTCISVHQFLGVCHPLCSLPYRTRRHAWLGTSTTWALVVL 180

Qy        181 QLLPTLAFSHTDYINGQMIWYDMTSQENFDRLFAYGIVLTLSGFLSLL 228
              ||||||||||||||||||||||||||||||||||||||||||||||||    |
Db        181 QLLPTLAFSHTDYINGQMIWYDMTSQENFDRLFAYGIVLTLSGFFPSL 228


RESULT 13
ADC86167
ID   ADC86167 standard; protein; 271 AA.
XX
AC   ADC86167;
XX
DT   01-JAN-2004  (first entry)
XX
DE   Human GPCR protein SEQ ID NO:620.
XX
KW   human; GPCR; guanosine triphosphate-binding protein coupled receptor;
KW   gene therapy.
XX
OS   Homo sapiens.
XX
PN   EP1270724-A2.
XX
PD   02-JAN-2003.
XX
PF   18-JUN-2002; 2002EP-00013517.
XX
PR   18-JUN-2001; 2001JP-00246789.
XX
PA   (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA   (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
XX
PI   Suwa M,  Asai K,  Akiyama Y,  Aburatani H;
XX
DR   WPI; 2003-315783/31.
DR   N-PSDB; ADC86166.
XX
PT   New polynucleotide, useful for preparing a composition for treating a
PT   patient in need of increased or suppressed activity or expression of the
PT   guanosine triphosphate-binding protein coupled receptor.
XX
PS   Claim 2; SEQ ID NO 620; 28pp; English.
XX
CC   The invention relates to a novel polynucleotide encoding a guanosine
CC   triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of
CC   the invention may have a use in gene therapy. The polynucleotide and
CC   polypeptide are useful for preparing a composition for treating a patient
CC   in need of increased or suppressed activity or expression of the
CC   guanosine triphosphate-binding protein coupled receptor. The protein
CC   sequences shown in ADC85549-ADC87617 represent GPCR's of the invention.
XX
SQ   Sequence 271 AA;

  Query Match             48.7%;  Score 942;  DB 7;  Length 271;
  Best Local Similarity   86.5%;  Pred. No. 3.8e-96;
  Matches  179;  Conservative    6;  Mismatches   22;  Indels    0;  Gaps    0;

Qy          29 MEKVDMNTSQEQGLCQFSEKYKQVYLSLAYSIIFILGLPLNGTVLWHSWGQTKRWSCATT 88
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 MEKVDMNTSQEQGLCQFSEKYKQVYLSLAYSIIFILGLPLNGTVLWHSWGQTKRWSCATT 60

Qy          89 YLVNLMVADLLYVLLPFLIITYSLDDRWPFGELLCKLVHFLFYINLYGSILLLTCISVHQ 148
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 YLVNLMVADLLYVLLPFLIITYSLDDRWPFGELLCKLVHFLFYINLYGSILLLTCISVHQ 120

Qy         149 FLGVCHPLCSLPYRTRRHAWLGTSTTWALVVLQLLPTLAFSHTDYINGQMIWYDMTSQEN 208
               ||||||||||||||||||||||||||||||||||||||||||||||||||  :  :||
Db         121 FLGVCHPLCSLPYRTRRHAWLGTSTTWALVVLQLLPTLAFSHTDYINGQMIWSLIKPEEN 180

Qy         209 FDRLFAYGIVLTLSGFLSLLGHFGVLF 235
                 |       ::   | : | | : |
Db         181 LMRTGNTARARSIRTILLVCGLFTLCF 207


RESULT 14
AAG80935
ID   AAG80935 standard; protein; 170 AA.
XX
AC   AAG80935;
XX
DT   28-AUG-2001  (first entry)
XX
DE   Human nGPCR12.
XX
KW   G protein-coupled receptor; nGPCR; seven transmembrane receptor;
KW   signal transduction; schizophrenia; thyroid disorder; renal failure;
KW   rheumatoid arthritis; CNS disorder; infection; metabolic disease;
KW   cardiovascular disease; proliferative disorder; hormonal disorder;
KW   neurological disorder; neuronal disorder; Alzheimer's disease; cancer;
KW   attention deficit-hyperactivity disorder/attention deficit disorder;
KW   Parkinson's disease; migraine; senile dementia; inflammatory disease;
KW   rheumatoid arthritis; autoimmune disorder; respiratory ailment;
KW   neuroprotective.
XX
OS   Homo sapiens.
XX
PN   WO200136473-A2.
XX
PD   25-MAY-2001.
XX
PF   16-NOV-2000; 2000WO-US031581.
XX
PR   16-NOV-1999;   99US-0165838P.
PR   17-NOV-1999;   99US-0166071P.
PR   19-NOV-1999;   99US-0166678P.
PR   28-DEC-1999;   99US-0173396P.
PR   22-FEB-2000; 2000US-0184129P.
PR   28-FEB-2000; 2000US-0185421P.
PR   28-FEB-2000; 2000US-0185554P.
PR   02-MAR-2000; 2000US-0186530P.
PR   03-MAR-2000; 2000US-0186811P.
PR   09-MAR-2000; 2000US-0188114P.
PR   17-MAR-2000; 2000US-0190310P.
PR   21-MAR-2000; 2000US-0190800P.
PR   20-APR-2000; 2000US-0198568P.
PR   02-MAY-2000; 2000US-0201190P.
PR   08-MAY-2000; 2000US-0203111P.
PR   25-MAY-2000; 2000US-0207094P.
XX
PA   (PHAA ) PHARMACIA & UPJOHN CO.
XX
PI   Vogeli G,  Wood LS,  Parodi LA,  Hiebsch RR,  Lind P,  Slightom J;
PI   Schellin KA,  Kaytes PS,  Bannigan CM,  Ruff V,  Sejlitz T,  Huff RM;
XX
DR   WPI; 2001-389826/41.
DR   N-PSDB; AAH50975.
XX
PT   New G protein-coupled receptor (nGPCR-x) and its encoding polynucleotide
PT   useful for diagnosing and treating e.g. schizophrenia.
XX
PS   Claim 37; Page 78; 261pp; English.
XX
CC   The present invention relates to novel G protein-coupled receptors
CC   (nGPCRx; where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27, 28,
CC   31-38, 40, 41, 53-60) and their coding sequences. The present sequence is
CC   one such G protein-coupled receptor. GPCRs are also known as seven
CC   transmembrane receptors and function in signal transduction. The nGPCRx
CC   coding sequences are useful for screening a human to diagnose a disorder
CC   affecting the brain or a genetic predisposition, specifically
CC   schizophrenia. nGPCRx are useful for identifying compounds useful for
CC   treating schizophrenia. Detection of nGPCRx in a sample is useful as a
CC   diagnostic tool for diseases or disorders e.g. thyroid disorders, renal
CC   failure, rheumatoid arthritis, CNS disorders, infections such as HIV-1,
CC   metabolic and cardiovascular diseases, proliferative disorders and
CC   hormonal disorders. Modulators of nGPCRx activity have the utility for
```

CC treating neurological disorders, including schizophrenia, ADHD/ADD
CC (attention deficit-hyperactivity disorder/attention deficit disorder),
CC and neuronal disorders such as Alzheimer's disease, Parkinson's disease,
CC migraine and senile dementia. Additional disorders include inflammatory
CC conditions (e.g. Crohn's disease), rheumatoid arthritis, autoimmune
CC disorders, cancers, respiratory ailments such as asthma, and inflammatory
CC diseases e.g. inflammatory bowel disease
XX
SQ Sequence 170 AA;

Query Match 47.6%; Score 921; DB 4; Length 170;
Best Local Similarity 100.0%; Pred. No. 4.4e-94;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy         83 WSCATTYLVNLMVADLLYVLLPFLIITYSLDDRWPFGELLCKLVHFLFYINLYGSILLLT 142
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 WSCATTYLVNLMVADLLYVLLPFLIITYSLDDRWPFGELLCKLVHFLFYINLYGSILLLT 60

Qy        143 CISVHQFLGVCHPLCSLPYRTRRHAWLGTSTTWALVVLQLLPTLAFSHTDYINGQMIWYD 202
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CISVHQFLGVCHPLCSLPYRTRRHAWLGTSTTWALVVLQLLPTLAFSHTDYINGQMIWYD 120

Qy        203 MTSQENFDRLFAYGIVLTLSGFLSLLGHFGVLFTDGQEPDQARGEPHEDR 252
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 MTSQENFDRLFAYGIVLTLSGFLSLLGHFGVLFTDGQEPDQARGEPHEDR 170
```

RESULT 15
ABG93753
ID ABG93753 standard; protein; 170 AA.
XX
AC ABG93753;
XX
DT 26-NOV-2002 (first entry)
XX
DE Human G protein-coupled receptor protein, beGPCR-seq12.
XX
KW Human; receptor; G protein-coupled receptor; GPCR; nGPCR; beGPCR;
KW nG protein coupled receptor; communication; serpentine structure;
KW seven transmembrane receptor; 7TM; mental disorder; diagnosis;
KW genetic predisposition; brain; immune response; gene therapy;
KW anxiety disorder; depression; bipolar disorder; schizophrenia;
KW Huntington's disease; dyskinesia; manic depression; stroke;
KW Parkinson's disease; Alzheimer's disease; diabetes; inflammation; wound;
KW tranquiliser.
XX
OS Homo sapiens.
XX
PN WO200264789-A1.
XX
PD 22-AUG-2002.
XX
PF 14-FEB-2001; 2001WO-US004641.
XX
PR 14-FEB-2001; 2001WO-US004641.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Lind P, Parodi LA, Vogeli G, Wood LS;
XX
DR WPI; 2002-674879/72.
DR N-PSDB; ABS70208.
XX
PT New nucleic acids and polypeptides of the nG protein-coupled receptor,
PT useful for treating or diagnosing a mental disorder or a disorder
PT affecting the brain, e.g. anxiety disorders, schizophrenia, stroke or
PT Parkinson's disease.
XX
PS Example 1; Page 73; 244pp; English.
XX
CC The invention discloses an isolated human polypeptide, and encoding
CC nucleic acid, for a G protein-coupled receptor (GPCR), particularly the
CC nG protein coupled receptor-14 (nGPCR-14). GPCRs are vital in the
CC communication between cells and their environment and are characterised
CC by a serpentine structure that passes through the cell membrane seven
CC times, hence the reason such receptors are sometimes called seven
CC transmembrane receptors (7TM). The polynucleotides and polypeptides are
CC useful for identifying an nGPCR allelic variant that correlates with a
CC mental disorder, for isolating an antibody that binds to an epitope of
CC the polypeptide, for identifying a compound that binds the polypeptide or
CC polynucleotide and/or modulates its biological activity, for screening a
CC human subject to diagnose a disorder, or a genetic predisposition to a
CC disorder, affecting the brain or a genetic disposition to the disorder,
CC for identifying compounds useful for the treatment of a mental disorder
CC and for identifying a compound useful as a modulator of binding between
CC nGPCR-14 and a binding partner of nGPCR-14. The polypeptide is also
CC useful for inducing an immune response in a mammal. The nucleic acid or
CC polypeptide is particularly useful, using gene therapy, for treating e.g.
CC anxiety disorders, depression, bipolar disorder, schizophrenia,
CC Huntington's disease, dyskinesias, manic depression, stroke, Parkinson's
CC disease or Alzheimer's disease. The nucleic acid and polypeptide may also
CC be used for treating diabetes, inflammation or wounds. The sequences
CC presented in ABG93747-ABG93793, ABG93795 and ABG93796 are the nGPCR (also
CC referred to as beGPCRs) proteins
XX
SQ Sequence 170 AA;

Query Match 47.6%; Score 921; DB 5; Length 170;
Best Local Similarity 100.0%; Pred. No. 4.4e-94;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         83 WSCATTYLVNLMVADLLYVLLPFLIITYSLDDRWPFGELLCKLVHFLFYINLYGSILLLT 142
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 WSCATTYLVNLMVADLLYVLLPFLIITYSLDDRWPFGELLCKLVHFLFYINLYGSILLLT 60

Qy        143 CISVHQFLGVCHPLCSLPYRTRRHAWLGTSTTWALVVLQLLPTLAFSHTDYINGQMIWYD 202
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CISVHQFLGVCHPLCSLPYRTRRHAWLGTSTTWALVVLQLLPTLAFSHTDYINGQMIWYD 120

Qy        203 MTSQENFDRLFAYGIVLTLSGFLSLLGHFGVLFTDGQEPDQARGEPHEDR 252
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 MTSQENFDRLFAYGIVLTLSGFLSLLGHFGVLFTDGQEPDQARGEPHEDR 170
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Search completed: November 4, 2004, 16:57:14
Job time : 159 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 4, 2004, 16:51:44 ; Search time 40 Seconds
(without alignments)
596.862 Million cell updates/sec

Title: US-10-763-972-2
Perfect score: 1936
Sequence: 1 MLSILLPSRGSRSGSRRGAL.....QNKLGEHPAGRKRCPGLNRS 360

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	421	21.7	374	4	US-09-745-842-15	Sequence 15, Appl
2	395	20.4	328	3	US-08-513-974B-39	Sequence 39, Appl
3	395	20.4	328	3	US-08-513-974B-371	Sequence 371, App
4	395	20.4	328	4	US-09-461-436B-39	Sequence 39, Appl
5	392.5	20.3	328	3	US-08-513-974B-56	Sequence 56, Appl
6	392.5	20.3	328	3	US-08-513-974B-380	Sequence 380, App
7	392.5	20.3	328	4	US-09-461-436B-56	Sequence 56, Appl
8	387.5	20.0	328	4	US-09-745-842-18	Sequence 18, Appl
9	387.5	20.0	377	4	US-09-745-842-17	Sequence 17, Appl
10	383.5	19.8	327	3	US-08-513-974B-372	Sequence 372, App
11	374.5	19.3	375	1	US-08-442-134A-2	Sequence 2, Appli
12	374.5	19.3	375	1	US-08-444-581B-2	Sequence 2, Appli
13	374.5	19.3	375	1	US-08-446-088A-2	Sequence 2, Appli
14	374.5	19.3	375	2	US-08-559-524A-3	Sequence 3, Appli
15	374.5	19.3	375	3	US-08-749-707-3	Sequence 3, Appli
16	374.5	19.3	375	4	US-09-947-922-3	Sequence 3, Appli
17	369	19.1	373	3	US-08-513-974B-373	Sequence 373, App
18	368.5	19.0	328	3	US-08-459-046-2	Sequence 2, Appli
19	368.5	19.0	328	4	US-09-102-710B-2	Sequence 2, Appli
20	367	19.0	365	4	US-09-745-842-16	Sequence 16, Appl
21	367	19.0	365	4	US-09-077-173D-2	Sequence 2, Appli
22	364.5	18.8	374	4	US-09-102-710B-3	Sequence 3, Appli
23	340	17.6	362	3	US-08-513-974B-374	Sequence 374, App
24	328	16.9	373	4	US-09-745-842-14	Sequence 14, Appl
25	326.5	16.9	373	2	US-08-559-524A-4	Sequence 4, Appli
26	326.5	16.9	373	3	US-08-749-707-4	Sequence 4, Appli
27	326.5	16.9	373	4	US-09-947-922-4	Sequence 4, Appli
28	274.5	14.2	302	2	US-08-467-948A-30	Sequence 30, Appl
29	274.5	14.2	302	3	US-08-467-947A-30	Sequence 30, Appl
30	273.5	14.1	344	2	US-08-467-948A-8	Sequence 8, Appli
31	273.5	14.1	344	3	US-08-467-947A-8	Sequence 8, Appli
32	258.5	13.4	370	3	US-08-781-250-2	Sequence 2, Appli
33	250.5	12.9	408	2	US-08-742-440A-6	Sequence 6, Appli
34	249	12.9	339	1	US-08-153-848-44	Sequence 44, Appl
35	249	12.9	339	2	US-08-812-871-3	Sequence 3, Appli
36	249	12.9	339	3	US-09-299-843A-44	Sequence 44, Appl
37	249	12.9	339	3	US-09-088-337B-44	Sequence 44, Appl
38	249	12.9	339	4	US-09-170-496D-32	Sequence 32, Appl
39	249	12.9	339	4	US-09-170-496D-182	Sequence 182, App
40	249	12.9	339	5	PCT-US93-11153-44	Sequence 44, Appl
41	249	12.9	339	5	PCT-US95-07180-2	Sequence 2, Appli
42	248.5	12.8	391	1	US-07-816-283-2	Sequence 2, Appli
43	248.5	12.8	391	1	US-08-417-103-2	Sequence 2, Appli
44	248.5	12.8	391	1	US-08-417-103-14	Sequence 14, Appl
45	246	12.7	347	4	US-08-405-271A-24	Sequence 24, Appl

ALIGNMENTS

RESULT 1
US-09-745-842-15
; Sequence 15, Application US/09745842
; Patent No. 6762029
; GENERAL INFORMATION:
; APPLICANT: Conley, Pamela B.
; APPLICANT: Jantzen, Hans-Michael
; APPLICANT: Ramakrishnan-DuBridge, Vanitha
; APPLICANT: Julius, David
; APPLICANT: Hollopeter, Gunter
; APPLICANT: COR Therapeutics, Inc.
; TITLE OF INVENTION: P2Y12 Receptor
; FILE REFERENCE: 44481-5053-US
; CURRENT APPLICATION NUMBER: US/09/745,842
; CURRENT FILING DATE: 2000-12-26
; PRIOR APPLICATION NUMBER: US 60/171,622
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Meleagris gallopavo
; FEATURE:
; OTHER INFORMATION: Turkey P2Y nucleotide receptor; tp2ynovel
US-09-745-842-15

Query Match 21.7%; Score 421; DB 4; Length 374;
Best Local Similarity 40.3%; Pred. No. 2.4e-29;
Matches 81; Conservative 40; Mismatches 72; Indels 8; Gaps 3;

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Qy          36 TSQEQGLCQFSEKYKQVYLSLAYSIIFILGLPLNGTVLWHSWGQTKRWSCATTYLVNLMV 95
               |:  :  | |:|::| : | ::| |:|::|||||   :|    : : |:  |||: || :
Db          26 TAAAEAKCVFNEEFKFILLPISYGIVFVVGLPLNSWAMWIFVSRMRPWNATTTYMFNLAI 85

Qy          96 ADLLYVL-LPFLIITYSLDDRWPFGELLCKLVHFLFYINLYGSILLLTCISVHQFLGVCH 154
               :| |||  || |:  |:  : ||||:: ||:| |||| ||| ||| ||||||:::|:||
Db          86 SDTLYVFSLPTLVYYYADRNNWPFGKVFCKIVRFLFYANLYSSILFLTCISVHRYMGICH 145

Qy         155 PLCSLPYRTRRHAWLGTSTTWALVVLQLLPTLAFSHTDYINGQMIWYDMTSQENFDRLFA 214
               |: || :   :|| |      | :| : |:| | |  |   :   : :| |  | ||
Db         146 PIRSLKWVKTKHARLICVGVWLVVTICLIPNLIFVTTSSKDNSTLCHDTTKPEEFDHYVH 205

Qy         215 YGIVLTLSGFLSLLGHFGVLF 235
               |      |  ::||  ||: |
Db         206 YS-----SSIMALL--FGIPF 219
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RESULT 2
US-08-513-974B-39

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; Sequence 39, Application US/08513974B
; Patent No. 6114139
;  GENERAL INFORMATION:
;    APPLICANT:  Hinuma, Shuji
;    APPLICANT:  Hosoya, Masaki
;    APPLICANT:  Fujii, Ryo
;    APPLICANT:  Ohtaki, Tetsuya
;    APPLICANT:  Fukusumi, Shoji
;    APPLICANT:  Ohgi, Kazuhiro
;    TITLE OF INVENTION:  G PROTEIN COUPLED RECEPTOR PROTEIN,
;    TITLE OF INVENTION:  PRODUCTION, AND USE THEREOF
;    NUMBER OF SEQUENCES:  380
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
;      STREET:  130 Water Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/513,974B
;      FILING DATE:  14-SEP-1995
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP95/01599
;      FILING DATE:  10-AUG-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 7-093989
;      FILING DATE:  19-AUG-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 7-057186
;      FILING DATE:  16-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 7-007177
;      FILING DATE:  20-JAN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 6-326611
;      FILING DATE:  28-DEC-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 6-270017
;      FILING DATE:  02-NOV-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 6-236357
;      FILING DATE:  30-SEP-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 6-236356
;      FILING DATE:  30-SEP-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 6-189274
;      FILING DATE:  11-AUG-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 6-189273
;      FILING DATE:  11-AUG-1945
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 6-189272
;      FILING DATE:  11-AUG-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Resnick, David S.
;      REGISTRATION NUMBER:  34,235
;      REFERENCE/DOCKET NUMBER:  45753
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-523-3400
;      TELEFAX:  617-523-6440
;  INFORMATION FOR SEQ ID NO:  39:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  328 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-513-974B-39

  Query Match             20.4%;  Score 395;  DB 3;  Length 328;
  Best Local Similarity   31.9%;  Pred. No. 4.2e-27;
  Matches  106;  Conservative   55;  Mismatches  137;  Indels   34;  Gaps    9;

Qy         29 MEKVDMNTSQEQGL----CQFSEKYKQVYLSLAYSIIFILGLPLNGTVLWHSWGQTKRWS 84
              ||: |  | |  ||    | : | :|:: |:  ||:: ::|||||  |:       : :
Db          1 MEQ-DNGTIQAPGLPPTTCVYREDFKRLLLTPVYSVVLVVGLPLNICVIAQICASRRTLT 59

Qy         85 CATTYLVNLMVADLLYVL-LPFLIITYSLDDRWPFGELLCKLVHFLFYINLYGSILLLTC 143
                :  | :|| :|||:|   || ||  |:  | ||||:| |: | |||| ||:|||| |||
Db         60 RSAVYTLNLALADLMYACSLPLLIYNYARGDHWPFGDLACRFVRFLFYANLHGSILFLTC 119

Qy        144 ISVHQFLGVCHPLCSLPYR-TRRHAWLGTSTTWALVVLQLLPTLAFSHTDYINGQMIWYD 202
              ||  ::||:|||| |   |  || ||:     | |  | |||  |: |     : : ||
Db        120 ISFQRYLGICHPLASWHKRGGRRAAWVVCGVVWLAVTAQCLPTAVFAATGIQRNRTVCYD 179

Qy        203 MTSQENFDRLFAYGIVLTLSGFL----SLLGHFGVLFTDGQEPDQARGEPHEDRQHSPSQ 258
              ::       |   ||: ||: |||    :||  :  :        |   |   ::|:   ::
Db        180 LSPPILSTRYLPYGMALTVIGFLLPFIALLACYCRMARRLCRQDGPAGPVAQERRSKAAR 239

Qy        259 VHPDHPTGVWPLHPLFCALPYHSLLLPHHLL-SAFSGLPALDGSQCGLQDMEASGECEQL 317
              :          :  |  :    || |:  :|:  : :  |  | : :  |:
Db        240 M-----------AVVVAAVFAISFLPFHITKTAYLAVRSTPGVSCPVLETFAAAYKGTR 287

Qy        318 PQPS------PVLSF----KGGKNRVRLLQKL 339
              |  |      |:| :    |  :    |||:|
Db        288 PFASVNSVLDPILFYFTQQKFRRQPHDLLQRL 319


RESULT 3
US-08-513-974B-371
; Sequence 371, Application US/08513974B
; Patent No. 6114139
;  GENERAL INFORMATION:
;    APPLICANT:  Hinuma, Shuji
;    APPLICANT:  Hosoya, Masaki
;    APPLICANT:  Fujii, Ryo
;    APPLICANT:  Ohtaki, Tetsuya
;    APPLICANT:  Fukusumi, Shoji
;    APPLICANT:  Ohgi, Kazuhiro
;    TITLE OF INVENTION:  G PROTEIN COUPLED RECEPTOR PROTEIN,
;    TITLE OF INVENTION:  PRODUCTION, AND USE THEREOF
;    NUMBER OF SEQUENCES:  380
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
;      STREET:  130 Water Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/513,974B
;      FILING DATE:  14-SEP-1995
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP95/01599
;      FILING DATE:  10-AUG-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 7-093989
;      FILING DATE:  19-AUG-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 7-057186
;      FILING DATE:  16-MAR-1995
;    PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: JP 7-007177
; FILING DATE: 20-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-326611
; FILING DATE: 28-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-270017
; FILING DATE: 02-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-236357
; FILING DATE: 30-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-236356
; FILING DATE: 30-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189274
; FILING DATE: 11-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189273
; FILING DATE: 11-AUG-1945
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189272
; FILING DATE: 11-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Resnick, David S.
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 45753
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; INFORMATION FOR SEQ ID NO: 371:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 328 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-513-974B-371

Query Match 20.4%; Score 395; DB 3; Length 328;
Best Local Similarity 31.9%; Pred. No. 4.2e-27;
Matches 106; Conservative 55; Mismatches 137; Indels 34; Gaps 9;

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Qy          29 MEKVDMNTSQEQGL----CQFSEKYKQVYLSLAYSIIFILGLPLNGTVLWHSWGQTKRWS 84
               ||: |  | |  ||    | : | :|:: |:  ||:: ::|||||  |:       :  :
Db           1 MEQ-DNGTIQAPGLPPTTCVYREDFKRLLLTPVYSVVLVVGLPLNICVIAQICASRRTLT 59

Qy          85 CATTYLVNLMVADLLYVL-LPFLIITYSLDDRWPFGELLCKLVHFLFYINLYGSILLLTC 143
                :  | :|| :|||:|   || ||  |:  | ||||:| |: | |||| ||:|||| |||
Db          60 RSAVYTLNLALADLMYACSLPLLIYNYARGDHWPFGDLACRFVRFLFYANLHGSILFLTC 119

Qy         144 ISVHQFLGVCHPLCSLPYR-TRRHAWLGTSTTWALVVLQLLPTLAFSHTDYINGQMIWYD 202
               ||  ::||:|||| |    |  || ||:     |  |  | |||  |: |     : : ||
Db         120 ISFQRYLGICHPLASWHKRGGRRAAWVVCGVVWLAVTAQCLPTAVFAATGIQRNRTVCYD 179

Qy         203 MTSQENFDRLFAYGIVLTLSGFL----SLLGHFGVLFTDGQEPDQARGEPHEDRQHSPSQ 258
               ::       |   ||: ||: |||    :||  :  :      |  |   ::|:   ::
Db         180 LSPPILSTRYLPYGMALTVIGFLLPFIALLACYCRMARRLCRQDGPAGPVAQERRSKAAR 239

Qy         259 VHPDHPTGVWPLHPLFCALPYHSLLLPHHLL-SAFSGLPALDGSQCGLQDMEASGECEQL 317
               :          :  |  :    || |:  :|:  : :  |  | : :  |:
Db         240 M-----------AVVVAAVFAISFLPFHITKTAYLAVRSTPGVSCPVLETFAAAYKGTR 287

Qy         318 PQPS------PVLSF----KGGKNRVRLLQKL 339
               |  |      |:| :    |  :    |||:|
Db         288 PFASVNSVLDPILFYFTQQKFRRQPHDLLQRL 319
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RESULT 4
US-09-461-436B-39
; Sequence 39, Application US/09461436B
; Patent No. 6538107
; GENERAL INFORMATION:
; APPLICANT: Shuji Hinuma
; Yasuaki Ito
; Ryo Fujii
; TITLE OF INVENTION: G Protein Coupled Receptor Protein,
; Production, And Use Thereof
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Edwards & Angell, LLP
; STREET: 101 Federal Street
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02209
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/461,436B
; FILING DATE: 14-Dec-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/513,974
; FILING DATE: 14-SEP-1995
; APPLICATION NUMBER: PCT/JP95/01599
; FILING DATE: 10-AUG-1995
; APPLICATION NUMBER: 7-093989
; FILING DATE: 19-APR-1995
; APPLICATION NUMBER: 7-057186
; FILING DATE: 16-MAR-1995
; APPLICATION NUMBER: 7-007177
; FILING DATE: 20-JAN-1995
; APPLICATION NUMBER: 6-326611
; FILING DATE: 28-DEC-1994
; APPLICATION NUMBER: 6-270017
; FILING DATE: 02-NOV-1994
; APPLICATION NUMBER: 6-236357
; FILING DATE: 30-SEP-1994
; APPLICATION NUMBER: 6-236356
; FILING DATE: 30-SEP-1994
; APPLICATION NUMBER: 6-189274
; FILING DATE: 11-AUG-1994
; APPLICATION NUMBER: 6-189273
; FILING DATE: 11-AUG-1994
; APPLICATION NUMBER: 6-189272
; FILING DATE: 11-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: CONLIN, DAVID G.
; REGISTRATION NUMBER: <Unknown>
; REFERENCE/DOCKET NUMBER: 45753 DIV2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-439-4444
; TELEFAX: 617-439-4170
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 328 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-461-436B-39

Query Match 20.4%; Score 395; DB 4; Length 328;
Best Local Similarity 31.9%; Pred. No. 4.2e-27;
Matches 106; Conservative 55; Mismatches 137; Indels 34; Gaps 9;

```
Qy          29 MEKVDMNTSQEQGL----CQFSEKYKQVYLSLAYSIIFILGLPLNGTVLWHSWGQTKRWS 84
               ||: |  | |  ||    | : | :|:: |:  ||:: ::|||||  |:       :  :
Db           1 MEQ-DNGTIQAPGLPPTTCVYREDFKRLLLTPVYSVVLVVGLPLNICVIAQICASRRTLT 59

Qy          85 CATTYLVNLMVADLLYVL-LPFLIITYSLDDRWPFGELLCKLVHFLFYINLYGSILLLTC 143
                :  | :|| :|||:|   || ||  |:  | ||||:| |: | |||| ||:|||| |||
```

```
Db          60 RSAVYTLNLALADLMYACSLPLLIYNYARGDHWPFGDLACRFVRFLFYANLHGSILFLTC 119

Qy         144 ISVHQPLGVCHPLCSLPYR-TRRHAWLGTSTTWALVVLQLLPTLAFSHTDYINGQMIWYD 202

Db         120 ISFQRYLGICHPLASWHKRGGRRAAWVVCGVVWLAVTAQCLPTAVFAATGIQRNRTVCYD 179

Qy         203 MTSQENFDRLFAYGIVLTLSGFL----SLLGHFGVLFTDGQEPDQARGEPHEDRQHSPSQ 258

Db         180 LSPPILSTRYLPYGMALTVIGFLLPFIALLACYCRMARRLCRQDGPAGPVAQERRSKAAR 239

Qy         259 VHPDHPTGVWPLHPLFCALPYHSLLLPHHLL-SAFSGLPALDGSQCGLQDMEASGECEQL 317

Db         240 M------------AVVVAAVFAISFLPFHITKTAYLAVRSTPGVSCPVLETFAAAYKGTR 287

Qy         318 PQPS------PVLSF----KGGKNRVRLLQKL 339

Db         288 PFASVNSVLDPILFYFTQQKFRRQPHDLLQRL 319


RESULT 5
US-08-513-974B-56
; Sequence 56, Application US/08513974B
; Patent No. 6114139
;  GENERAL INFORMATION:
;    APPLICANT:  Hinuma, Shuji
;    APPLICANT:  Hosoya, Masaki
;    APPLICANT:  Fujii, Ryo
;    APPLICANT:  Ohtaki, Tetsuya
;    APPLICANT:  Fukusumi, Shoji
;    APPLICANT:  Ohgi, Kazuhiro
;    TITLE OF INVENTION:  G PROTEIN COUPLED RECEPTOR PROTEIN,
;    TITLE OF INVENTION:  PRODUCTION, AND USE THEREOF
;    NUMBER OF SEQUENCES:  380
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
;      STREET:  130 Water Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/513,974B
;      FILING DATE:  14-SEP-1995
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP95/01599
;      FILING DATE:  10-AUG-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 7-093989
;      FILING DATE:  19-AUG-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 7-057186
;      FILING DATE:  16-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 7-007177
;      FILING DATE:  20-JAN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 6-326611
;      FILING DATE:  28-DEC-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 6-270017
;      FILING DATE:  02-NOV-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 6-236357
;      FILING DATE:  30-SEP-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 6-236356
;      FILING DATE:  30-SEP-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 6-189274
;      FILING DATE:  11-AUG-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 6-189273
;      FILING DATE:  11-AUG-1945
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 6-189272
;      FILING DATE:  11-AUG-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Resnick, David S.
;      REGISTRATION NUMBER:  34,235
;      REFERENCE/DOCKET NUMBER:  45753
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-523-3400
;      TELEFAX:  617-523-6440
;  INFORMATION FOR SEQ ID NO:  56:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  328 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-513-974B-56

  Query Match             20.3%;  Score 392.5;  DB 3;  Length 328;
  Best Local Similarity   33.0%;  Pred. No. 6.9e-27;
  Matches  109;  Conservative   42;  Mismatches  142;  Indels   37;  Gaps    9;

Qy          33 DMNTSQEQGL----CQFSEKYKQVYLSLAYSIIFILGLPLNGTVLWHSWGQTKRWSCATT 88

Db           4 DNGTGQALGLPPTTCVYRENFKQLLLPPVYSAVLAAGLPLNICVITQICTSRRALTRTAV 63

Qy          89 YLVNLMVADLLYVL-LPFLIITYSLDDRWPFGELLCKLVHFLFYINLYGSILLLTCISVH 147

Db          64 YTLNLALADLLYACSLPLLIYNYAQGDHWPFGDFACRLVRFLFYANLHGSILFLTCISFQ 123

Qy         148 QFLGVCHPLCSLPYR-TRRHAWLGTSTTWALVVLQLLPTLAFSHTDYINGQMIWYDMTSQ 206

Db         124 RYLGICHPLAPWHKRGGRRAAWLVCVTVWLAVTTQCLPTAIFAATGIQRNRTVCYDLSPP 183

Qy         207 ENFDRLFAYGIVLTLSGFL----SLLGHFGVLFTDGQEPDQARGEPHEDRQHSPSQVHPD 262

Db         184 ALATHYMPYGMALTVIGFLLPFAALLACYCLLAC-----------RLCRQDGPAEPVAQ 231

Qy         263 HPTGVWPLHPLFCALPYHSLLLPHHLL-SAFSGLPALDGSQCGLQDMEASGECEQLPQP- 320

Db         232 ERRGKAARMAVVVAAAFAISFLPFHITKTAYLAVGSTPGVPCTV--LEAFAAAYKGTRPF 289

Qy         321 -------SPVLSF----KGGKNRVRLLQKL 339

Db         290 ASANSVLDPILFYFTQKKFRRRPHELLQKL 319


RESULT 6
US-08-513-974B-380
; Sequence 380, Application US/08513974B
; Patent No. 6114139
;  GENERAL INFORMATION:
;    APPLICANT:  Hinuma, Shuji
;    APPLICANT:  Hosoya, Masaki
;    APPLICANT:  Fujii, Ryo
;    APPLICANT:  Ohtaki, Tetsuya
;    APPLICANT:  Fukusumi, Shoji
;    APPLICANT:  Ohgi, Kazuhiro
;    TITLE OF INVENTION:  G PROTEIN COUPLED RECEPTOR PROTEIN,
;    TITLE OF INVENTION:  PRODUCTION, AND USE THEREOF
;    NUMBER OF SEQUENCES:  380
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
;      STREET:  130 Water Street
;      CITY:  Boston
;      STATE:  MA
```

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;       COUNTRY:  USA
;       ZIP:  02109
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/513,974B
;       FILING DATE:  14-SEP-1995
;       CLASSIFICATION:  536
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/JP95/01599
;       FILING DATE:  10-AUG-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 7-093989
;       FILING DATE:  19-AUG-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 7-057186
;       FILING DATE:  16-MAR-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 7-007177
;       FILING DATE:  20-JAN-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 6-326611
;       FILING DATE:  28-DEC-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 6-270017
;       FILING DATE:  02-NOV-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 6-236357
;       FILING DATE:  30-SEP-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 6-236356
;       FILING DATE:  30-SEP-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 6-189274
;       FILING DATE:  11-AUG-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 6-189273
;       FILING DATE:  11-AUG-1945
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 6-189272
;       FILING DATE:  11-AUG-1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Resnick, David S.
;       REGISTRATION NUMBER:  34,235
;       REFERENCE/DOCKET NUMBER:  45753
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  617-523-3400
;       TELEFAX:  617-523-6440
;   INFORMATION FOR SEQ ID NO:  380:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  328 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-513-974B-380

  Query Match           20.3%;  Score 392.5;  DB 3;  Length 328;
  Best Local Similarity   33.0%;  Pred. No. 6.9e-27;
  Matches  109;  Conservative   42;  Mismatches  142;  Indels   37;  Gaps    9;

Qy         33 DMNTSQEQGL----CQFSEKYKQVYLSLAYSIIFILGLPLNGTVLWHSWGQTKRWSCATT 88
              |  | |  ||     | : | :||: |   || :   |||||  |:       :  :
Db          4 DNGTGQALGLPPTTCVYRENFKQLLLPPVYSAVLAAGLPLNICVITQICTSRRALTRTAV 63

Qy         89 YLVNLMVADLLYVL-LPFLIITYSLDDRWPFGELLCKLVHFLFYINLYGSILLLTCISVH 147
              | :|| :|||||   || ||  |:  | ||||:  |:|| |||| ||:|||| |||||
Db         64 YTLNLALADLLYACSLPLLIYNYAQGDHWPFGDFACRLVRFLFYANLHGSILFLTCISFQ 123

Qy        148 QFLGVCHPLCSLPYR-TRRHAWLGTSTTWALVVLQLLPTLAFSHTDYINGQMIWYDMTSQ 206
             ::||:||||      |  || |||   | |  |  | |||  |: |     : : ||::

Db        124 RYLGICHPLAPWHKRGGRRAAWLVCVTVWLAVTTQCLPTAIFAATGIQRNRTVCYDLSPP 183

Qy        207 ENFDRLFAYGIVLTLSGFL----SLLGHFGVLFTDGQEPDQARGEPHEDRQHSPSQVHPD 262
                 ||: ||: |||    :||  : :|                  ||  |::
Db        184 ALATHYMPYGMALTVIGFLLPFAALLACYCLLAC-----------RLCRQDGPAEPVAQ 231

Qy        263 HPTGVWPLHPLFCALPYHSLLLPHHLL-SAFSGLPALDGSQCGLQDMEASGECEQLPQP- 320
                |     :  |  :    || |:  :|:  : :  |  | :  :||     :  :|
Db        232 ERRGKAARMAVVVAAAFAISFLPFHITKTAYLAVGSTPGVPCTV--LEAFAAAYKGTRPF 289

Qy        321 -------SPVLSF----KGGKNRVRLLQKL 339
                    |:| :    |  :    |||||
Db        290 ASANSVLDPILFYFTQKKFRRRPHELLQKL 319


RESULT 7
US-09-461-436B-56
; Sequence 56, Application US/09461436B
; Patent No. 6538107
;   GENERAL INFORMATION:
;       APPLICANT: Shuji Hinuma
;                  Yasuaki Ito
;                  Ryo Fujii
;       TITLE OF INVENTION: G Protein Coupled Receptor Protein,
;                           Production, And Use Thereof
;       NUMBER OF SEQUENCES: 61
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Edwards & Angell, LLP
;            STREET: 101 Federal Street
;            CITY: BOSTON
;            STATE: MA
;            COUNTRY: USA
;            ZIP: 02209
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/461,436B
;            FILING DATE: 14-Dec-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/513,974
;            FILING DATE: 14-SEP-1995
;            APPLICATION NUMBER: PCT/JP95/01599
;            FILING DATE: 10-AUG-1995
;            APPLICATION NUMBER: 7-093989
;            FILING DATE: 19-APR-1995
;            APPLICATION NUMBER: 7-057186
;            FILING DATE: 16-MAR-1995
;            APPLICATION NUMBER: 7-007177
;            FILING DATE: 20-JAN-1995
;            APPLICATION NUMBER: 6-326611
;            FILING DATE: 28-DEC-1994
;            APPLICATION NUMBER: 6-270017
;            FILING DATE: 02-NOV-1994
;            APPLICATION NUMBER: 6-236357
;            FILING DATE: 30-SEP-1994
;            APPLICATION NUMBER: 6-236356
;            FILING DATE: 30-SEP-1994
;            APPLICATION NUMBER: 6-189274
;            FILING DATE: 11-AUG-1994
;            APPLICATION NUMBER: 6-189273
;            FILING DATE: 11-AUG-1994
;            APPLICATION NUMBER: 6-189272
;            FILING DATE: 11-AUG-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: CONLIN, DAVID G.
;            REGISTRATION NUMBER: <Unknown>
;            REFERENCE/DOCKET NUMBER: 45753 DIV2
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 617-439-4444
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;             TELEFAX: 617-439-4170
;   INFORMATION FOR SEQ ID NO: 56:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 328 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: peptide
;        SEQUENCE DESCRIPTION: SEQ ID NO: 56:
US-09-461-436B-56

  Query Match            20.3%;  Score 392.5;  DB 4;  Length 328;
  Best Local Similarity  33.0%;  Pred. No. 6.9e-27;
  Matches  109;  Conservative   42;  Mismatches  142;  Indels   37;  Gaps    9;

Qy         33 DMNTSQEQGL----CQFSEKYKQVYLSLAYSIIFILGLPLNGTVLWHSWGQTKRWSCATT 88
              |  | |  ||    | : | :||: |   || :   |||||  |:       :  :
Db          4 DNGTGQALGLPPTTCVYRENFKQLLLPPVYSAVLAAGLPLNICVITQICTSRRALTRTAV 63

Qy         89 YLVNLMVADLLYVL-LPFLIITYSLDDRWPFGELLCKLVHFLFYINLYGSILLLTCISVH 147
              | :|| :|||||   || ||  |:  | ||||:  |:|| |||| ||:|||| |||||
Db         64 YTLNLALADLLYACSLPLLIYNYAQGDHWPFGDFACRLVRFLFYANLHGSILFLTCISFQ 123

Qy        148 QFLGVCHPLCSLPYR-TRRHAWLGTSTTWALVVLQLLPTLAFSHTDYINGQMIWYDMTSQ 206
              ::||:||||      |  || |||   | |  |  | |||  |: |     : : ||::
Db        124 RYLGICHPLAPWHKRGGRRAAWLVCVTVWLAVTTQCLPTAIFAATGIQRNRTVCYDLSPP 183

Qy        207 ENFDRLFAYGIVLTLSGFL----SLLGHFGVLFTDGQEPDQARGEPHEDRQHSPSQVHPD 262
                  ||: ||: |||    :||  : :|                 ||  |::
Db        184 ALATHYMPYGMALTVIGFLLPFAALLACYCLLAC-----------RLCRQDGPAEPVAQ 231

Qy        263 HPTGVWPLHPLFCALPYHSLLLPHHLL-SAFSGLPALDGSQCGLQDMEASGECEQLPQP- 320
                 |      :  |  :    || |:  :|:  : :  |  | :  :||     :  :|
Db        232 ERRGKAARMAVVVAAAFAISFLPFHITKTAYLAVGSTPGVPCTV--LEAFAAAYKGTRPF 289

Qy        321 -------SPVLSF----KGGKNRVRLLQKL 339
                    |:| :    |  :    |||||
Db        290 ASANSVLDPILFYFTQKKFRRRPHELLQKL 319


RESULT 8
US-09-745-842-18
; Sequence 18, Application US/09745842
; Patent No. 6762029
; GENERAL INFORMATION:
;  APPLICANT:  Conley, Pamela B.
;  APPLICANT:  Jantzen, Hans-Michael
;  APPLICANT:  Ramakrishnan-DuBridge, Vanitha
;  APPLICANT:  Julius, David
;  APPLICANT:  Hollopeter, Gunter
;  APPLICANT:  COR Therapeutics, Inc.
;  TITLE OF INVENTION:  P2Y12 Receptor
;  FILE REFERENCE:  44481-5053-US
;  CURRENT APPLICATION NUMBER: US/09/745,842
;  CURRENT FILING DATE:  2000-12-26
;  PRIOR APPLICATION NUMBER:  US 60/171,622
;  PRIOR FILING DATE:  1999-12-23
;  NUMBER OF SEQ ID NOS:  21
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 18
;   LENGTH: 328
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: P2Y6 receptor
US-09-745-842-18

  Query Match            20.0%;  Score 387.5;  DB 4;  Length 328;
  Best Local Similarity  32.7%;  Pred. No. 1.9e-26;
  Matches  108;  Conservative   42;  Mismatches  143;  Indels   37;  Gaps    9;

Qy         33 DMNTSQEQGL----CQFSEKYKQVYLSLAYSIIFILGLPLNGTVLWHSWGQTKRWSCATT 88
              |  | |  ||    | : | :||: |   || :   |||||  |:       :  :
Db          4 DNGTGQALGLPPTTCVYRENFKQLLLPPVYSAVLAAGLPLNICVITQICTSRRALTRTAV 63

Qy         89 YLVNLMVADLLYVL-LPFLIITYSLDDRWPFGELLCKLVHFLFYINLYGSILLLTCISVH 147
              | :|| :|||||   || ||  |:  | ||||:  |:|| |||| ||:|||| |||||
Db         64 YTLNLALADLLYACSLPLLIYNYAQGDHWPFGDFACRLVRFLFYANLHGSILFLTCISFQ 123

Qy        148 QFLGVCHPLCSLPYR-TRRHAWLGTSTTWALVVLQLLPTLAFSHTDYINGQMIWYDMTSQ 206
              ::||:||||      |  || |||   | |  |  | |||  |: |     : : ||::
Db        124 RYLGICHPLAPWHKRGGRRAAWLVCVTVWLAVTTQCLPTAIFAATGIQRNRTVCYDLSPP 183

Qy        207 ENFDRLFAYGIVLTLSGFL----SLLGHFGVLFTDGQEPDQARGEPHEDRQHSPSQVHPD 262
                  ||: ||: |||    :||  : :|                 ||  |::
Db        184 ALATHYMPYGMALTVIGFLLPFAALLACYCLLAC-----------RLCRQDGPAEPVAQ 231

Qy        263 HPTGVWPLHPLFCALPYHSLLLPHHLL-SAFSGLPALDGSQCGLQDMEASGECEQLPQP- 320
                 |      :  |  :    || |:  :|:  : :  |  | :  :||     :  :|
Db        232 ERRGKAARMAVVVAAAFAISFLPFHITKTAYLAVGSTPGVPCTV--LEAFAAAYKGTRPF 289

Qy        321 -------SPVLSF----KGGKNRVRLLQKL 339
                    |:| :    |  :    |||||
Db        290 ASANSVLDPILFYFTQKKFRRRPHELLQKL 319


Db          4 DNGTGQALGLPPTTCVYRENFKQLLLPPVYSAVLAAGLPLNICVITQICTSRRALTRTAV 63

Qy         89 YLVNLMVADLLYVL-LPFLIITYSLDDRWPFGELLCKLVHFLFYINLYGSILLLTCISVH 147
              | :|| :|||||   || ||  |:  | ||||:  |:|| |||| ||:|||| |||||
Db         64 YTLNLALADLLYACSLPLLIYNYAQGDHWPFGDFACRLVRFLFYANLHGSILFLTCISFQ 123

Qy        148 QFLGVCHPLCSLPYR-TRRHAWLGTSTTWALVVLQLLPTLAFSHTDYINGQMIWYDMTSQ 206
              ::||:||||      |  || |||   | |  |  | |||  |: |     : : ||::
Db        124 RYLGICHPLAPWHKRGGRRAAWLVCVAVWLAVTTQCLPTAIFAATGIQRNRTVCYDLSPP 183

Qy        207 ENFDRLFAYGIVLTLSGFL----SLLGHFGVLFTDGQEPDQARGEPHEDRQHSPSQVHPD 262
                  ||: ||: |||    :||  : :|                 ||  |::
Db        184 ALATHYMPYGMALTVIGFLLPFAALLACYCLLAC-----------RLCRQDGPAEPVAQ 231

Qy        263 HPTGVWPLHPLFCALPYHSLLLPHHLL-SAFSGLPALDGSQCGLQDMEASGECEQLPQP- 320
                 |      :  |  :    || |:  :|:  : :  |  | :  :||     :  :|
Db        232 ERRGKAARMAVVVAAAFAISFLPFHITKTAYLAVRSTPGVPCTV--LEAFAAAYKGTRPF 289

Qy        321 -------SPVLSF----KGGKNRVRLLQKL 339
                    |:| :    |  :    |||||
Db        290 ASANSVLDPILFYFTQKKFRRRPHELLQKL 319


RESULT 9
US-09-745-842-17
; Sequence 17, Application US/09745842
; Patent No. 6762029
; GENERAL INFORMATION:
;  APPLICANT:  Conley, Pamela B.
;  APPLICANT:  Jantzen, Hans-Michael
;  APPLICANT:  Ramakrishnan-DuBridge, Vanitha
;  APPLICANT:  Julius, David
;  APPLICANT:  Hollopeter, Gunter
;  APPLICANT:  COR Therapeutics, Inc.
;  TITLE OF INVENTION:  P2Y12 Receptor
;  FILE REFERENCE:  44481-5053-US
;  CURRENT APPLICATION NUMBER: US/09/745,842
;  CURRENT FILING DATE:  2000-12-26
;  PRIOR APPLICATION NUMBER:  US 60/171,622
;  PRIOR FILING DATE:  1999-12-23
;  NUMBER OF SEQ ID NOS:  21
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 17
;   LENGTH: 377
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: P2Y2 purinergic receptor; p2ur
US-09-745-842-17

  Query Match            20.0%;  Score 387.5;  DB 4;  Length 377;
  Best Local Similarity  32.7%;  Pred. No. 2.3e-26;
  Matches  117;  Conservative   41;  Mismatches  119;  Indels   81;  Gaps   13;

Qy         43 CQFSEKYKQVYLSLAYSIIFILGLPLNGTVLWHSWGQTKRWSCATTYLVNLMVADLLYVL 102
              |:|:| :| | | ::| :: :||| ||    |:    : | |: :|||: :| |:| ||
Db         25 CRFNEDFKYVLLPVSYGVVCVLGLCLNAVALYIFLCRLKTWNASTTYMFHLAVSDALYAA 84

Qy        103 -LPFLIITYSLDDRWPFGELLCKLVHFLFYINLYGSILLLTCISVHQFLGVCHPLCSLPY 161
               || |:  |:  | |||  :||||| |||| ||| ||| |||||||: |||  || || :
Db         85 SLPLLVYYYARGDHWPFSTVLCKLVRFLFYTNLYCSILFLTCISVHRCLGVLRPLRSLRW 144

Qy        162 RTRRHAWLGTSTTWALVVLQLLPTLAFSHTDYINGQMIWYDMTSQENFDRLFAYGIVLTL 221
               |:|       | ||:   | | |  |    |::  :| :: | | |  ||  |:
Db        145 GRARYARRVAGAVWVLVLACQAPVLYFVTTSARGGRVTCHDTSAPELFSRFVAYSSVM-- 202

Qy        222 SGFLSLLGHFGVLF-------------------TDGQEPDQARGEPHEDRQHSPSQVHP 261
              | ||  | | |                    | |        | |   |:  :
Db        203 ---LGLL--FAVPFAVILVCYVLMARRLLKPAYGTSG-------GLPRAKRKSVRT---- 246

Qy        262 DHPTGVWPLHPLF--CALPYH----------SLLLPHHLLSAFS-----GLPALDGSQCG 304
                  :  :|  | ||:|           || |  | |:| :        |    : |
Db        247 -----IAVVLAVFALCFLPFHVTRTLYYSFRSLDLSCHTLNAINMAYKVTRPLASANSC- 300
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Qy        305 LQDMEASGECEQLPQPSPVLSFKGGKNRVRLLQKLRQNKLGEHPA--GRKRCPGLNRS 360
                                                                  
Db        301 ---------------LDPVLYFLAGQRLVRFARDAKP-PTGPSPATPARRRL-GLRRS 341


RESULT 10
US-08-513-974B-372
; Sequence 372, Application US/08513974B
; Patent No. 6114139
;  GENERAL INFORMATION:
;    APPLICANT:  Hinuma, Shuji
;    APPLICANT:  Hosoya, Masaki
;    APPLICANT:  Fujii, Ryo
;    APPLICANT:  Ohtaki, Tetsuya
;    APPLICANT:  Fukusumi, Shoji
;    APPLICANT:  Ohgi, Kazuhiro
;    TITLE OF INVENTION:  G PROTEIN COUPLED RECEPTOR PROTEIN,
;    TITLE OF INVENTION:  PRODUCTION, AND USE THEREOF
;    NUMBER OF SEQUENCES:  380
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
;      STREET:  130 Water Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/513,974B
;      FILING DATE:  14-SEP-1995
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP95/01599
;      FILING DATE:  10-AUG-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 7-093989
;      FILING DATE:  19-AUG-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 7-057186
;      FILING DATE:  16-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 7-007177
;      FILING DATE:  20-JAN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 6-326611
;      FILING DATE:  28-DEC-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 6-270017
;      FILING DATE:  02-NOV-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 6-236357
;      FILING DATE:  30-SEP-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 6-236356
;      FILING DATE:  30-SEP-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 6-189274
;      FILING DATE:  11-AUG-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 6-189273
;      FILING DATE:  11-AUG-1945
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 6-189272
;      FILING DATE:  11-AUG-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Resnick, David S.
;      REGISTRATION NUMBER:  34,235
;      REFERENCE/DOCKET NUMBER:  45753
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-523-3400
;      TELEFAX:  617-523-6440
;  INFORMATION FOR SEQ ID NO:  372:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  327 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-513-974B-372

  Query Match           19.8%;  Score 383.5;  DB 3;  Length 327;
  Best Local Similarity   40.9%;  Pred. No. 4.3e-26;
  Matches   83;  Conservative   32;  Mismatches   81;  Indels    7;  Gaps    4;

Qy         29 MEKVDMNTSQEQGL----CQFSEKYKQVYLSLAYSIIFILGLPLNGTVLWHSWGQTKRWS 84
                ||: |  | |  ||    | : | :|:: |:  ||:: ::|||||  |:       :  :
Db          1 MEQ-DNGTIQAPGLPPTTCVYREDFKRLLLTPVYSVVLVVGLPLNICVIAQICASRRTLT 59

Qy         85 CATTYLVNLMVADLLYVL-LPFLIITYSLDDRWPFGELLCKLVHFLFYINLYGSILLLTC 143
                :  | :|| :|||:|   || ||  |:  | ||||:| |: | |||| ||:|||| |||
Db         60 RSAVYTLNLALADLMYACSLPLLIYNYARCDHWPFGDLACRFVRFLFYANLHGSILFLTC 119

Qy        144 ISVHQFLGVCHPLCSLPYR-TRRHAWLGTSTTWALVVLQLLPTLAFSHTDYINGQMIWYD 202
                ||  ::||:|||| |   |  || ||:      |  |  | | |  |: |     : : ||
Db        120 ISFQRYLGICHPLASWHKRGGRRAAWVVCGVVWLAVTAQCLRTAVFAATGIQRNRTVCYD 179

Qy        203 MTSQENFDRLFAYGIVLTLSGFL 225
                ::     |   ||: ||: |||
Db        180 LSPPILSTRYLPYGMALTVIGFL 202


RESULT 11
US-08-442-134A-2
; Sequence 2, Application US/08442134A
; Patent No. 5596088
;  GENERAL INFORMATION:
;    APPLICANT:  Boucher, Richard C.
;    APPLICANT:  Weisman, Gary A.
;    APPLICANT:  Turner, John T.
;    APPLICANT:  Harden, Thomas K.
;    APPLICANT:  Parr, Claude E.
;    APPLICANT:  Sullivan, Daniel M.
;    APPLICANT:  Erb, Laura
;    APPLICANT:  Lustig, Kevin D.
;    TITLE OF INVENTION:  DNA Encoding the Human P2U Receptor and
;    TITLE OF INVENTION:  Null Cells Expressing P2U Receptors
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Bell, Seltzer, Park & Gibson
;      STREET:  Post Office Drawer 34009
;      CITY:  Charlotte
;      STATE:  No. 5596088th Carolina
;      COUNTRY:  USA
;      ZIP:  28234
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/442,134A
;      FILING DATE:  16-MAY-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sibley, Kenneth D.
;      REGISTRATION NUMBER:  31,665
;      REFERENCE/DOCKET NUMBER:  5470-71A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  919-420-2200
;      TELEFAX:  919-881-3175
;  INFORMATION FOR SEQ ID NO:  2:
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;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  375 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-442-134A-2

  Query Match           19.3%;  Score 374.5;  DB 1;  Length 375;
  Best Local Similarity   32.7%;  Pred. No. 3.2e-25;
  Matches  115;  Conservative   43;  Mismatches  123;  Indels   71;  Gaps   13;

Qy         43 CQFSEKYKQVYLSLAYSIIFILGLPLNGTVLWHSWGQTKRWSCATTYLVNLMVADLLYVL 102
              |:|:| :| | | ::| :: :||| ||   |:    : | |: :|||: :| |:| ||
Db         25 CRFNEDFKYVLLPVSYGVVCVLGLCLNAVGLYIFLCRLKTWNASTTYMFHLAVSDALYAA 84

Qy        103 -LPFLIITYSLDDRWPFGELLCKLVHFLFYINLYGSILLLTCISVHQFLGVCHPLCSLPY 161
               || |:  |:  | |||  :|||| |||| ||| ||| |||||||: |||  || || :
Db         85 SLPLLVYYYARGDHWPFSTVLCKLVRFLFYTNLYCSILFLTCISVHRCLGVLRPLRSLRW 144

Qy        162 RTRRHAWLGTSTTWALVVLQLLPTLAFSHTDYINGQMIWYDMTSQENFDRLFAYGIVLTL 221
              |:|       | ||:    | | | |    | :  :| :: | | |  ||  |:
Db        145 GRARYARRVAGAVWVLVLACQAPVLYFVTTS-ARGPLTCHDTSAPELFSRFVAYSSVM-- 201

Qy        222 SGFLSLLGHFGVLF-------------------TDGQEPDQARGEPHEDRQHSPSQVHP 261
              | ||  | | |                     | |       | |   |:  :
Db        202 ---LGLL--FAVPFAVILVCYVLMARRLLKPAYGTSG-------GLPRAKRKSVRT---- 245

Qy        262 DHPTGVWPLHPLF--CALPYH----------SLLLPHHLLSAFSGLPALDGSQCGLQDME 309
                  :  :  :|  | ||:|          || |  | |:| :          :  :
Db        246 -----IAVVLAVFALCFLPFHVTRTLYYSFRSLDLSCHTLNAIN-------MAYKVTRLA 293

Qy        310 ASGECEQLPQPSPVLSFKGGKNRVRLLQKLRQNKLGEHPA-GRKRCPGLNRS 360
              ::  |      ||| |  |:  ||  :  :    |  ||  :|  || ||
Db        294 SANSC-----LDPVLYFLAGQRLVRFARDAKP-PTGPSPATPARRTLGLRRS 339


RESULT 12
US-08-444-581B-2
; Sequence 2, Application US/08444581B
; Patent No. 5607836
;  GENERAL INFORMATION:
;    APPLICANT:  Boucher, Richard C.
;    APPLICANT:  Weisman, Gary A.
;    APPLICANT:  Turner, John T.
;    APPLICANT:  Harden, Thomas K.
;    APPLICANT:  Parr, Claude E.
;    APPLICANT:  Sullivan, Daniel M.
;    APPLICANT:  Erb, Laura
;    APPLICANT:  Lustig, Kevin D.
;    TITLE OF INVENTION:  DNA Encoding the Human P2U Receptor and
;    TITLE OF INVENTION:  Null Cells Expressing P2U Receptors
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Bell, Seltzer, Park & Gibson
;      STREET:  Post Office Drawer 34009
;      CITY:  Charlotte
;      STATE:  No. 5607836th Carolina
;      COUNTRY:  USA
;      ZIP:  28234
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/444,581B
;      FILING DATE:  19-MAY-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/442,134
;      FILING DATE:  16-MAY-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sibley, Kenneth D.
;      REGISTRATION NUMBER:  31,665
;      REFERENCE/DOCKET NUMBER:  5470-71A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  919-420-2200
;      TELEFAX:  919-881-3175
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  375 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-444-581B-2

  Query Match           19.3%;  Score 374.5;  DB 1;  Length 375;
  Best Local Similarity   32.7%;  Pred. No. 3.2e-25;
  Matches  115;  Conservative   43;  Mismatches  123;  Indels   71;  Gaps   13;

Qy         43 CQFSEKYKQVYLSLAYSIIFILGLPLNGTVLWHSWGQTKRWSCATTYLVNLMVADLLYVL 102
              |:|:| :| | | ::| :: :||| ||   |:    : | |: :|||: :| |:| ||
Db         25 CRFNEDFKYVLLPVSYGVVCVLGLCLNAVGLYIFLCRLKTWNASTTYMFHLAVSDALYAA 84

Qy        103 -LPFLIITYSLDDRWPFGELLCKLVHFLFYINLYGSILLLTCISVHQFLGVCHPLCSLPY 161
               || |:  |:  | |||  :|||| |||| ||| ||| |||||||: |||  || || :
Db         85 SLPLLVYYYARGDHWPFSTVLCKLVRFLFYTNLYCSILFLTCISVHRCLGVLRPLRSLRW 144

Qy        162 RTRRHAWLGTSTTWALVVLQLLPTLAFSHTDYINGQMIWYDMTSQENFDRLFAYGIVLTL 221
              |:|       | ||:    | | | |    | :  :| :: | | |  ||  |:
Db        145 GRARYARRVAGAVWVLVLACQAPVLYFVTTS-ARGPLTCHDTSAPELFSRFVAYSSVM-- 201

Qy        222 SGFLSLLGHFGVLF-------------------TDGQEPDQARGEPHEDRQHSPSQVHP 261
              | ||  | | |                     | |       | |   |:  :
Db        202 ---LGLL--FAVPFAVILVCYVLMARRLLKPAYGTSG-------GLPRAKRKSVRT---- 245

Qy        262 DHPTGVWPLHPLF--CALPYH----------SLLLPHHLLSAFSGLPALDGSQCGLQDME 309
                  :  :  :|  | ||:|          || |  | |:| :          :  :
Db        246 -----IAVVLAVFALCFLPFHVTRTLYYSFRSLDLSCHTLNAIN-------MAYKVTRLA 293

Qy        310 ASGECEQLPQPSPVLSFKGGKNRVRLLQKLRQNKLGEHPA-GRKRCPGLNRS 360
              ::  |      ||| |  |:  ||  :  :    |  ||  :|  || ||
Db        294 SANSC-----LDPVLYFLAGQRLVRFARDAKP-PTGPSPATPARRTLGLRRS 339


RESULT 13
US-08-446-088A-2
; Sequence 2, Application US/08446088A
; Patent No. 5691156
;  GENERAL INFORMATION:
;    APPLICANT:  Boucher, Richard C.
;    APPLICANT:  Weisman, Gary A.
;    APPLICANT:  Turner, John T.
;    APPLICANT:  Harden, Thomas K.
;    APPLICANT:  Parr, Claude E.
;    APPLICANT:  Sullivan, Daniel M.
;    APPLICANT:  Erb, Laura
;    APPLICANT:  Lustig, Kevin D.
;    TITLE OF INVENTION:  DNA Encoding the Human P2U Receptor and
;    TITLE OF INVENTION:  Null Cells Expressing P2U Receptors
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Bell, Seltzer, Park & Gibson
;      STREET:  Post Office Drawer 34009
;      CITY:  Charlotte
;      STATE:  No. 5691156th Carolina
;      COUNTRY:  USA
;      ZIP:  28234
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/446,088A
;      FILING DATE:  19-MAY-1995
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; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kenneth D. Sibley
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5470-71C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-420-2200
; TELEFAX: 919-881-3175
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 375 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-446-088A-2

Query Match 19.3%; Score 374.5; DB 1; Length 375;
Best Local Similarity 32.7%; Pred. No. 3.2e-25;
Matches 115; Conservative 43; Mismatches 123; Indels 71; Gaps 13;

```
Qy         43 CQFSEKYKQVYLSLAYSIIFILGLPLNGTVLWHSWGQTKRWSCATTYLVNLMVADLLYVL 102
              |:|:| :| | | ::| :: :||| ||   |:    : | |: :|||: :| |:| ||
Db         25 CRFNEDFKYVLLPVSYGVVCVLGLCLNAVGLYIFLCRLKTWNASTTYMFHLAVSDALYAA 84

Qy        103 -LPFLIITYSLDDRWPFGELLCKLVHFLFYINLYGSILLLTCISVHQFLGVCHPLCSLPY 161
               || |:  |:  | |||  :||||| |||| ||| ||| ||||||| ||| || || :
Db         85 SLPLLVYYYARGDHWPFSTVLCKLVRFLFYTNLYCSILFLTCISVHRCLGVLRPLRSLRW 144

Qy        162 RTRRHAWLGTSTTWALVVLQLLPTLAFSHTDYINGQMIWYDMTSQENFDRLFAYGIVLTL 221
              |:|       | ||:    | | |  |    | :  :| :: | | |  ||  |:
Db        145 GRARYARRVAGAVWVLVLACQAPVLYFVTTS-ARGPLTCHDTSAPELFSRFVAYSSVM-- 201

Qy        222 SGFLSLLGHFGVLF-------------------TDGQEPDQARGEPHEDRQHSPSQVHP 261
              | ||  | | |                    | |     | |  |:  :
Db        202 ---LGLL--FAVPFAVILVCYVLMARRLLKPAYGTSG-------GLPRAKRKSVRT---- 245

Qy        262 DHPTGVWPLHPLF--CALPYH----------SLLLPHHLLSAFSGLPALDGSQCGLQDME 309
                :  :  :|  | ||:|           || |  | |:| :         :  :
Db        246 -----IAVVLAVFALCFLPFHVTRTLYYSFRSLDLSCHTLNAIN-------MAYKVTRLA 293

Qy        310 ASGECEQLPQPSPVLSFKGGKNRVRLLQKLRQNKLGEHPA-GRKRCPGLNRS 360
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Db        294 SANSC-----LDPVLYFLAGQRLVRFARDAKP-PTGPSPATPARRTLGLRRS 339
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RESULT 14
US-08-559-524A-3
; Sequence 3, Application US/08559524A
; Patent No. 5871963
; GENERAL INFORMATION:
; APPLICANT: Conley, Pamela B.
; APPLICANT: Jantzen, Hans-Michael
; TITLE OF INVENTION: NOVEL PURINERGIC RECEPTOR
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
; STREET: 1800 M Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5869
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/559,524A
; FILING DATE: 15-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Adler, Reid G.
; REGISTRATION NUMBER: 30,988
; REFERENCE/DOCKET NUMBER: 044481-5010-00-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-467-7000
; TELEFAX: 202-467-7176
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 375 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-559-524A-3

Query Match 19.3%; Score 374.5; DB 2; Length 375;
Best Local Similarity 32.7%; Pred. No. 3.2e-25;
Matches 115; Conservative 43; Mismatches 123; Indels 71; Gaps 13;

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Qy         43 CQFSEKYKQVYLSLAYSIIFILGLPLNGTVLWHSWGQTKRWSCATTYLVNLMVADLLYVL 102
              |:|:| :| | | ::| :: :||| ||   |:    : | |: :|||: :| |:| ||
Db         25 CRFNEDFKYVLLPVSYGVVCVLGLCLNAVGLYIFLCRLKTWNASTTYMFHLAVSDALYAA 84

Qy        103 -LPFLIITYSLDDRWPFGELLCKLVHFLFYINLYGSILLLTCISVHQFLGVCHPLCSLPY 161
               || |:  |:  | |||  :||||| |||| ||| ||| ||||||| ||| || || :
Db         85 SLPLLVYYYARGDHWPFSTVLCKLVRFLFYTNLYCSILFLTCISVHRCLGVLRPLRSLRW 144

Qy        162 RTRRHAWLGTSTTWALVVLQLLPTLAFSHTDYINGQMIWYDMTSQENFDRLFAYGIVLTL 221
              |:|       | ||:    | | |  |    | :  :| :: | | |  ||  |:
Db        145 GRARYARRVAGAVWVLVLACQAPVLYFVTTS-ARGPLTCHDTSAPELFSRFVAYSSVM-- 201

Qy        222 SGFLSLLGHFGVLF-------------------TDGQEPDQARGEPHEDRQHSPSQVHP 261
              | ||  | | |                    | |     | |  |:  :
Db        202 ---LGLL--FAVPFAVILVCYVLMARRLLKPAYGTSG-------GLPRAKRKSVRT---- 245

Qy        262 DHPTGVWPLHPLF--CALPYH----------SLLLPHHLLSAFSGLPALDGSQCGLQDME 309
                :  :  :|  | ||:|           || |  | |:| :         :  :
Db        246 -----IAVVLAVFALCFLPFHVTRTLYYSFRSLDLSCHTLNAIN-------MAYKVTRLA 293

Qy        310 ASGECEQLPQPSPVLSFKGGKNRVRLLQKLRQNKLGEHPA-GRKRCPGLNRS 360
              ::  |       ||| |  |: ||  :  :    |  ||   :|  || ||
Db        294 SANSC-----LDPVLYFLAGQRLVRFARDAKP-PTGPSPATPARRTLGLRRS 339
```

RESULT 15
US-08-749-707-3
; Sequence 3, Application US/08749707
; Patent No. 6063582
; GENERAL INFORMATION:
; APPLICANT: Conley, Pamela B.
; APPLICANT: Jantzen, Hans-Michael
; TITLE OF INVENTION: NOVEL PURINERGIC RECEPTOR
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
; STREET: 1800 M Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5869
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/749,707
; FILING DATE: 15-NOV-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Adler, Reid G.
; REGISTRATION NUMBER: 30,988
; REFERENCE/DOCKET NUMBER: 044481-5010-01-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-467-7000

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;      TELEFAX:  202-467-7176
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  375 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-749-707-3

  Query Match             19.3%;  Score 374.5;  DB 3;  Length 375;
  Best Local Similarity   32.7%;  Pred. No. 3.2e-25;
  Matches  115;  Conservative   43;  Mismatches  123;  Indels   71;  Gaps   13;

Qy         43 CQFSEKYKQVYLSLAYSIIFILGLPLNGTVLWHSWGQTKRWSCATTYLVNLMVADLLYVL 102
              |:|:|  :| | | ::| :: :||| ||   |:    : | |: :|||: :| |:| ||
Db         25 CRFNEDFKYVLLPVSYGVVCVLGLCLNAVGLYIFLCRLKTWNASTTYMFHLAVSDALYAA 84

Qy        103 -LPFLIITYSLDDRWPFGELLCKLVHFLFYINLYGSILLLTCISVHQFLGVCHPLCSLPY 161
               || |:  |:  | |||  :|||| |||| ||| ||| |||||||: |||  || || :
Db         85 SLPLLVYYYARGDHWPFSTVLCKLVRFLFYTNLYCSILFLTCISVHRCLGVLRPLRSLRW 144

Qy        162 RTRRHAWLGTSTTWALVVLQLLPTLAFSHTDYINGQMIWYDMTSQENFDRLFAYGIVLTL 221
              |:|       | ||:   | | |   |   | :  :| :: | | |  ||  |:
Db        145 GRARYARRVAGAVWVLVLACQAPVLYFVTTS-ARGPLTCHDTSAPELFSRFVAYSSVM-- 201

Qy        222 SGFLSLLGHFGVLF--------------------TDGQEPDQARGEPHEDRQHSPSQVHP 261
                | ||  | | |                   | |       | |   |:   :
Db        202 ---LGLL--FAVPFAVILVCYVLMARRLLKPAYGTSG-------GLPRAKRKSVRT---- 245

Qy        262 DHPTGVWPLHPLF--CALPYH----------SLLLPHHLLSAFSGLPALDGSQCGLQDME 309
                  :  :  :|  | ||:|          || |  | |:| :          :  :
Db        246 -----IAVVLAVFALCFLPFHVTRTLYYSFRSLDLSCHTLNAIN-------MAYKVTRLA 293

Qy        310 ASGECEQLPQPSPVLSFKGGKNRVRLLQKLRQNKLGEHPA-GRKRCPGLNRS 360
              ::  |       ||| |  |:  ||  :  :    |  ||   :|  || ||
Db        294 SANSC-----LDPVLYFLAGQRLVRFARDAKP-PTGPSPATPARRTLGLRRS 339


Search completed: November  4, 2004, 17:02:01
Job time : 42 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 4, 2004, 16:54:39 ; Search time 141 Seconds
(without alignments)
901.853 Million cell updates/sec

Title: US-10-763-972-2
Perfect score: 1936
Sequence: 1 MLSILLPSRGSRSGSRRGAL.....QNKLGEHPAGRKRCPGLNRS 360

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1566620 seqs, 353225886 residues

Total number of hits satisfying chosen parameters: 1566620

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
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18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1936	100.0	360	14	US-10-023-586B-2	Sequence 2, Appli
2	1936	100.0	360	16	US-10-763-972-2	Sequence 2, Appli
3	1798	92.9	333	14	US-10-088-726-20	Sequence 20, Appl
4	1542	79.6	295	14	US-10-275-910-2	Sequence 2, Appli
5	1529	79.0	361	15	US-10-072-012-166	Sequence 166, App
6	1189	61.4	338	10	US-09-885-453-4	Sequence 4, Appli
7	1189	61.4	338	14	US-10-079-384-6	Sequence 6, Appli
8	1185	61.2	339	14	US-10-023-586B-4	Sequence 4, Appli
9	1185	61.2	339	15	US-10-333-946-1	Sequence 1, Appli
10	1185	61.2	339	16	US-10-763-972-4	Sequence 4, Appli
11	942	48.7	271	14	US-10-017-161-708	Sequence 708, App
12	942	48.7	271	14	US-10-292-798-620	Sequence 620, App
13	921	47.6	170	10	US-09-782-974C-14	Sequence 14, Appl
14	447	23.1	328	14	US-10-010-568-10	Sequence 10, Appl
15	447	23.1	328	14	US-10-010-568-14	Sequence 14, Appl
16	447	23.1	328	14	US-10-275-910-3	Sequence 3, Appli
17	447	23.1	328	14	US-10-375-157-10	Sequence 10, Appl
18	447	23.1	328	14	US-10-375-157-14	Sequence 14, Appl
19	447	23.1	328	15	US-10-072-012-519	Sequence 519, App
20	447	23.1	328	15	US-10-072-012-520	Sequence 520, App
21	421	21.7	374	10	US-09-745-842-15	Sequence 15, Appl
22	421	21.7	374	14	US-10-010-568-11	Sequence 11, Appl
23	421	21.7	374	14	US-10-375-157-11	Sequence 11, Appl
24	421	21.7	374	15	US-10-072-012-518	Sequence 518, App
25	416	21.5	537	14	US-10-311-956-4	Sequence 4, Appli
26	416	21.5	537	14	US-10-010-568-12	Sequence 12, Appl
27	416	21.5	537	14	US-10-375-157-12	Sequence 12, Appl
28	416	21.5	537	15	US-10-055-569A-52	Sequence 52, Appl
29	416	21.5	537	15	US-10-072-012-517	Sequence 517, App
30	395	20.4	328	14	US-10-278-087A-39	Sequence 39, Appl
31	392.5	20.3	328	14	US-10-278-087A-56	Sequence 56, Appl
32	388	20.0	361	10	US-09-964-821B-15	Sequence 15, Appl
33	388	20.0	361	14	US-10-010-568-9	Sequence 9, Appli
34	388	20.0	361	14	US-10-268-332-15	Sequence 15, Appl
35	388	20.0	361	14	US-10-375-157-9	Sequence 9, Appli
36	388	20.0	361	15	US-10-072-012-521	Sequence 521, App
37	388	20.0	361	17	US-10-775-965-15	Sequence 15, Appl
38	387.5	20.0	328	10	US-09-745-842-18	Sequence 18, Appl
39	387.5	20.0	328	14	US-10-225-567A-223	Sequence 223, App
40	387.5	20.0	328	14	US-10-354-358-10	Sequence 10, Appl
41	387.5	20.0	328	14	US-10-295-027-1288	Sequence 1288, Ap
42	387.5	20.0	377	10	US-09-745-842-17	Sequence 17, Appl
43	387.5	20.0	377	14	US-10-225-567A-217	Sequence 217, App
44	374.5	19.3	375	9	US-09-947-922-3	Sequence 3, Appli
45	374.5	19.3	375	16	US-10-706-532-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-10-023-586B-2
; Sequence 2, Application US/10023586B
; Publication No. US20030166882A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Ltd. (EP (GB) only)
; APPLICANT: Pfizer Inc. (US, JP, EP except GB)
; APPLICANT: Fidock, Mark David
; TITLE OF INVENTION: No. US20030166882A1el Polypeptide
; FILE REFERENCE: PC10960AGPR
; CURRENT APPLICATION NUMBER: US/10/023,586B
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: GB 0030855.1
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 60/260,563
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: US 60/265,688
; PRIOR FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: GB 0101222.8
; PRIOR FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-023-586B-2

Query Match 100.0%; Score 1936; DB 14; Length 360;
Best Local Similarity 100.0%; Pred. No. 3.9e-176;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
US-10-763-972-2
; Sequence 2, Application US/10763972
; Publication No. US20040137500A1
; GENERAL INFORMATION:
;  APPLICANT: PFIZER INC.
;  APPLICANT:  Fidock, Mark David
;  TITLE OF INVENTION: Novel Polypeptide
;  FILE REFERENCE: PC10960B
;  CURRENT APPLICATION NUMBER: US/10/763,972
;  CURRENT FILING DATE:  2004-01-23
;  PRIOR APPLICATION NUMBER: GB 0030855.1
;  PRIOR FILING DATE: 2000-12-18
;  PRIOR APPLICATION NUMBER: US 60/260,563
;  PRIOR FILING DATE: 2001-01-09
;  PRIOR APPLICATION NUMBER: US 60/265,688
;  PRIOR FILING DATE: 2001-02-01
;  PRIOR APPLICATION NUMBER: GB 0101222.8
;  PRIOR FILING DATE: 2001-01-17
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
;   LENGTH: 360
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-763-972-2

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Qy         121 LLCKLVHFLFYINLYGSILLLTCISVHQFLGVCHPLCSLPYRTRRHAWLGTSTTWALVVL 180
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Db         121 LLCKLVHFLFYINLYGSILLLTCISVHQFLGVCHPLCSLPYRTRRHAWLGTSTTWALVVL 180

Qy         181 QLLPTLAFSHTDYINGQMIWYDMTSQENFDRLFAYGIVLTLSGFLSLLGHFGVLFTDGQE 240
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Qy         241 PDQARGEPHEDRQHSPSQVHPDHPTGVWPLHPLFCALPYHSLLLPHHLLSAFSGLPALDG 300
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Qy         301 SQCGLQDMEASGECEQLPQPSPVLSFKGGKNRVRLLQKLRQNKLGEHPAGRKRCPGLNRS 360
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RESULT 3
US-10-088-726-20
; Sequence 20, Application US/10088726
; Publication No. US20030157558A1
; GENERAL INFORMATION:
;  APPLICANT: Matsumoto et al.
;  TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE-BINDING PROTEIN-COUPLED RECEPTORS ANI
;  TITLE OF INVENTION:  THEREOF, AND PRODUCTION AND USES THEREOF
;  FILE REFERENCE: 62514
;  CURRENT APPLICATION NUMBER: US/10/088,726
;  CURRENT FILING DATE:  2002-03-22
;  PRIOR APPLICATION NUMBER: PCT/JP00/09408
;  PRIOR FILING DATE: 2000-12-28
;  PRIOR APPLICATION NUMBER: JP   1999-375152
;  PRIOR FILING DATE: 1999-12-28
;  PRIOR APPLICATION NUMBER: JP   2000-101339
;  PRIOR FILING DATE: 2000-03-31
;  NUMBER OF SEQ ID NOS: 63
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
;   LENGTH: 333
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-088-726-20

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RESULT 4
US-10-275-910-2
; Sequence 2, Application US/10275910
; Publication No. US20030166142A1
; GENERAL INFORMATION:
;  APPLICANT: Ramakrishnan, Shyam
;  TITLE OF INVENTION: REGULATION OF HUMAN P2Y-LIKE G PROTEIN-COUPLED RECEPTOR
;  FILE REFERENCE: 4974.00885
;  CURRENT APPLICATION NUMBER: US/10/275,910
;  CURRENT FILING DATE:  2002-11-12
;  PRIOR APPLICATION NUMBER: US 60/203,582
;  PRIOR FILING DATE: 2000-05-11
;  PRIOR APPLICATION NUMBER: US 60/269,857
;  PRIOR FILING DATE: 2001-02-21
;  NUMBER OF SEQ ID NOS: 6
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;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 295
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-275-910-2

  Query Match             79.6%;  Score 1542;  DB 14;  Length 295;
  Best Local Similarity   98.6%;  Pred. No. 1.3e-138;
  Matches  284;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         29 MEKVDMNTSQEQGLCQFSEKYKQVYLSLAYSIIFILGLPLNGTVLWHSWGQTKRWSCATT 88
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Qy         89 YLVNLMVADLLYVLLPFLIITYSLDDRWPFGELLCKLVHFLFYINLYGSILLLTCISVHQ 148
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Db         61 YLVNLMVADLLYVLLPFLIITYSLDDRWPFGELLCKLVHFLFYINLYGSILLLTCISVHQ 120

Qy        149 FLGVCHPLCSLPYRTRRHAWLGTSTTWALVVLQLLPTLAFSHTDYINGQMIWYDMTSQEN 208
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Db        181 FDRLFAYGIVLTLSGFLSLLGHFGVLFTDGQEPDQARGEPHEDRQHSPSQVHPDHPTGVW 240

Qy        269 PLHPLFCALPYHSLLLPHHLLSAFSGLPALDGSQCGLQDMEASGECEQ 316
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Db        241 PLHPLFCALPYHSLLLPHHLLSAFSGLPALDGSQCGLQDMEASVKAMQ 288


RESULT 5
US-10-072-012-166
; Sequence 166, Application US/10072012
; Publication No. US20040033493A1
; GENERAL INFORMATION:
;  APPLICANT: Tchernev, Velizar
;  APPLICANT:  Spytek, Kimberly
;  APPLICANT:  Zerhusen, Bryan
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Shimkets, Richard
;  APPLICANT:  Li, Li
;  APPLICANT:  Gangolli, Esha
;  APPLICANT:  Padigaru, Muralidhara
;  APPLICANT:  Anderson, David W.
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Miller, Charles E.
;  APPLICANT:  Gerlach, Valerie
;  APPLICANT:  Taupier Jr, Raymond J.
;  APPLICANT:  Gusev, Vladimir Y.
;  APPLICANT:  Colman, Steven D.
;  APPLICANT:  Wolenc, Adam R.
;  APPLICANT:  Pena, Carol E. A
;  APPLICANT:  Furtak, Katarzyna
;  APPLICANT:  Grosse, William M.
;  APPLICANT:  Alsobrook II, John P.
;  APPLICANT:  Lepley, Denise M.
;  APPLICANT:  Rieger, Daniel K.
;  APPLICANT:  Burgess, Catherine E.
;  TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
;  FILE REFERENCE: 21402-258
;  CURRENT APPLICATION NUMBER: US/10/072,012
;  CURRENT FILING DATE:  2002-01-31
;  PRIOR APPLICATION NUMBER: 60/265,102
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: 60/265,514
;  PRIOR FILING DATE: 2001-01-31
;  PRIOR APPLICATION NUMBER: 60/265,517
;  PRIOR FILING DATE: 2001-01-31
;  PRIOR APPLICATION NUMBER: 60/265,412
;  PRIOR FILING DATE: 2001-01-31
;  PRIOR APPLICATION NUMBER: 60/265,395
;  PRIOR FILING DATE: 2001-01-31
;  PRIOR APPLICATION NUMBER: 60/266,406
;  PRIOR FILING DATE: 2001-02-02
;  PRIOR APPLICATION NUMBER: 60/266,767
;  PRIOR FILING DATE: 2001-02-05
;  PRIOR APPLICATION NUMBER: 60/267,057
;  PRIOR FILING DATE: 2001-02-07
;  PRIOR APPLICATION NUMBER: 60/266,975
;  PRIOR FILING DATE: 2001-02-07
;  PRIOR APPLICATION NUMBER: 60/267,459
;  PRIOR FILING DATE: 2001-02-08
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 1391
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 166
;   LENGTH: 361
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-072-012-166

  Query Match             79.0%;  Score 1529;  DB 15;  Length 361;
  Best Local Similarity   82.6%;  Pred. No. 2.9e-137;
  Matches  303;  Conservative   11;  Mismatches   39;  Indels   14;  Gaps    5;

Qy          1 MLSILLPSRGSRSGSRRGALLLEGASRDMEKVDMNTSQEQGLCQFSEKYKQVYLSLAYSI 60
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Db          1 MLSILLPSRGSRSGSRRGALLLEGASRDMEKVDMNTSQEQGLCQFSEKYKQVYLSLAYSI 60

Qy         61 IFILGLPLNGTVLWHSWGQTKRWSCATTYLVNLMVADLLYVLLPFLIITYSLDDRWPFGE 120
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Db         61 IFILGLPLNGTVLWHSWGQTKRWSCATTYLVNLMVADLLYVLLPFLIITYSLDDRWPFGE 120

Qy        121 LLCKLVHFLFYINLYGSILLLTCISVHQFLGVCHPLCSLPYRTRRHAWLGTSTTWALVVL 180
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Db        121 LLCKLVHFLFYINLYGSILLLTCISVHQFLGVCHPLCSLPYRTRRHAWLGTSTTWALVVL 180

Qy        181 QLLPTLAFSHTDYINGQMIWYDMTSQENFDRLFAYGIVLTLSGFLSLLGHFGVLFTDGQE 240
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Db        181 QLLPTLAFSHTDYINGQMIWYDMTSQENFDRLFAYGIVLTLSGFLSLLGHFGVYSL---- 236

Qy        241 PDQARG--EPHEDRQHSPSQVHPDHPTGVWPLHPLF--CALPYHSLLLPHHLLSAF---S 293
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Db        237 --MVRSLIKPEENLMRTGNTARARSIRTILLVCGLFTLCFVPFH-ITRSFYLTICFLLSQ 293

Qy        294 GLPALDGSQCGLQDMEASGECEQLPQPSPVLSFKGGKNRVRLLQKLRQNKLGEHPAGRKR 353
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Db        294 DCQLLMAAQCGLQDMEASGECEQLPQPSPVLSFKGGKNRVRLLQKLRQNKLGEHPAGRKR 353

Qy        354 CPGLNRS 360
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Db        354 CPGLNRS 360


RESULT 6
US-09-885-453-4
; Sequence 4, Application US/09885453
; Publication No. US20030088080A1
; GENERAL INFORMATION:
;  APPLICANT: Communi, Didier
;  TITLE OF INVENTION: RECEPTOR GPCRx10
;  FILE REFERENCE: 9409/2082
;  CURRENT APPLICATION NUMBER: US/09/885,453
;  CURRENT FILING DATE:  2001-06-20
;  PRIOR APPLICATION NUMBER: US 09/885,453
;  PRIOR FILING DATE: 2001-06-21
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 338
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: Amino acid sequence
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;   LOCATION: (1)..(338)
;   OTHER INFORMATION: GPCRx6 amino acid sequence
US-09-885-453-4

  Query Match             61.4%;  Score 1189;  DB 10;  Length 338;
  Best Local Similarity   98.7%;  Pred. No. 8.1e-105;
  Matches  225;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 MLSILLPSRGSRSGSRRGALLLEGASRDMEKVDMNTSQEQGLCQFSEKYKQVYLSLAYSI 60
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Qy         61 IFILGLPLNGTVLWHSWGQTKRWSCATTYLVNLMVADLLYVLLPFLIITYSLDDRWPFGE 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 IFILGLPLNGTVLWHSWGQTKRWSCATTYLVNLMVADLLYVLLPFLIITYSLDDRWPFGE 120

Qy        121 LLCKLVHFLFYINLYGSILLLTCISVHQFLGVCHPLCSLPYRTRRHAWLGTSTTWALVVL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLCKLVHFLFYINLYGSILLLTCISVHQFLGVCHPLCSLPYRTRRHAWLGTSTTWALVVL 180

Qy        181 QLLPTLAFSHTDYINGQMIWYDMTSQENFDRLFAYGIVLTLSGFLSLL 228
              |||||||||||||||||||||||||||||||||||||||||||||    |
Db        181 QLLPTLAFSHTDYINGQMIWYDMTSQENFDRLFAYGIVLTLSGFFPSL 228


RESULT 7
US-10-079-384-6
; Sequence 6, Application US/10079384
; Publication No. US20030108986A1
; GENERAL INFORMATION:
;  APPLICANT: Communi, Didier
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS COMPRISING G-PROTEIN COUPLED RECEPTORS
;  FILE REFERENCE: 9409/2132
;  CURRENT APPLICATION NUMBER: US/10/079,384
;  CURRENT FILING DATE:  2002-02-20
;  PRIOR APPLICATION NUMBER: US 09/885,453
;  PRIOR FILING DATE: 2001-06-20
;  NUMBER OF SEQ ID NOS: 50
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
;   LENGTH: 338
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-079-384-6

  Query Match             61.4%;  Score 1189;  DB 14;  Length 338;
  Best Local Similarity   98.7%;  Pred. No. 8.1e-105;
  Matches  225;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 MLSILLPSRGSRSGSRRGALLLEGASRDMEKVDMNTSQEQGLCQFSEKYKQVYLSLAYSI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLSILLPSRGSRSGSRRGALLLEGASRDMEKVDMNTSQEQGLCQFSEKYKQVYLSLAYSI 60

Qy         61 IFILGLPLNGTVLWHSWGQTKRWSCATTYLVNLMVADLLYVLLPFLIITYSLDDRWPFGE 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 IFILGLPLNGTVLWHSWGQTKRWSCATTYLVNLMVADLLYVLLPFLIITYSLDDRWPFGE 120

Qy        121 LLCKLVHFLFYINLYGSILLLTCISVHQFLGVCHPLCSLPYRTRRHAWLGTSTTWALVVL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLCKLVHFLFYINLYGSILLLTCISVHQFLGVCHPLCSLPYRTRRHAWLGTSTTWALVVL 180

Qy        181 QLLPTLAFSHTDYINGQMIWYDMTSQENFDRLFAYGIVLTLSGFLSLL 228
              |||||||||||||||||||||||||||||||||||||||||||||    |
Db        181 QLLPTLAFSHTDYINGQMIWYDMTSQENFDRLFAYGIVLTLSGFFPSL 228


RESULT 8
US-10-023-586B-4
; Sequence 4, Application US/10023586B
; Publication No. US20030166882A1
; GENERAL INFORMATION:
;  APPLICANT: Pfizer Ltd. (EP (GB) only)
;  APPLICANT:  Pfizer Inc. (US, JP, EP except GB)
;  APPLICANT:  Fidock, Mark David
;  TITLE OF INVENTION: No. US20030166882A1el Polypeptide
;  FILE REFERENCE: PC10960AGPR
;  CURRENT APPLICATION NUMBER: US/10/023,586B
;  CURRENT FILING DATE:  2001-12-18
;  PRIOR APPLICATION NUMBER: GB 0030855.1
;  PRIOR FILING DATE: 2000-12-18
;  PRIOR APPLICATION NUMBER: US 60/260,563
;  PRIOR FILING DATE: 2001-01-09
;  PRIOR APPLICATION NUMBER: US 60/265,688
;  PRIOR FILING DATE: 2001-02-01
;  PRIOR APPLICATION NUMBER: GB 0101222.8
;  PRIOR FILING DATE: 2001-01-17
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 339
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-023-586B-4

  Query Match             61.2%;  Score 1185;  DB 14;  Length 339;
  Best Local Similarity   99.6%;  Pred. No. 1.9e-104;
  Matches  225;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MLSILLPSRGSRSGSRRGALLLEGASRDMEKVDMNTSQEQGLCQFSEKYKQVYLSLAYSI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLSILLPSRGSRSGSRRGALLLEGASRDMEKVDMNTSQEQGLCQFSEKYKQVYLSLAYSI 60

Qy         61 IFILGLPLNGTVLWHSWGQTKRWSCATTYLVNLMVADLLYVLLPFLIITYSLDDRWPFGE 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 IFILGLPLNGTVLWHSWGQTKRWSCATTYLVNLMVADLLYVLLPFLIITYSLDDRWPFGE 120

Qy        121 LLCKLVHFLFYINLYGSILLLTCISVHQFLGVCHPLCSLPYRTRRHAWLGTSTTWALVVL 180
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        121 LLCKLVHFLFYINLYGSILLLTCISVHQFLGVWHPLCSLPYRTRRHAWLGTSTTWALVVL 180

Qy        181 QLLPTLAFSHTDYINGQMIWYDMTSQENFDRLFAYGIVLTLSGFLS 226
              |||||||||||||||||||||||||||||||||||||||||||||
Db        181 QLLPTLAFSHTDYINGQMIWYDMTSQENFDRLFAYGIVLTLSGFLS 226


RESULT 9
US-10-333-946-1
; Sequence 1, Application US/10333946
; Publication No. US20040023252A1
; GENERAL INFORMATION:
;  APPLICANT: INCYTE GENOMICS, INC.; THORNTON, Michael B.
;  APPLICANT:  ARVIZU, Chandra S.; LAL, Preeti G.
;  APPLICANT:  BURFORD, Neil; YUE, Henry
;  APPLICANT:  GANDHI, Ameena R.; ELLIOTT, Vicki S.
;  APPLICANT:  RAMKUMAR, Jayalaxmi; BAUGHN, Mariah R.
;  APPLICANT:  KALLICK, Deborah A.; CHAWLA, Narinder K.
;  APPLICANT:  HAFALIA, April J.A.; YAO, Monique G.
;  APPLICANT:  LU, Yan; TRIBOULEY, Catherine M.
;  APPLICANT:  POLICKY, Jennifer L.; KEARNEY, Liam
;  APPLICANT:  GRAUL, Richard C.; WARREN, Bridget A.
;  APPLICANT:  LEE, Ernestine A.; DING, Li
;  TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
;  FILE REFERENCE: PI-0176 USN
;  CURRENT APPLICATION NUMBER: US/10/333,946
;  CURRENT FILING DATE:  2003-01-22
;  PRIOR APPLICATION NUMBER: PCT/US01/23433
;  PRIOR FILING DATE: 2001-07-25
;  PRIOR APPLICATION NUMBER: US 60/221,478
;  PRIOR FILING DATE: 2000-07-27
;  PRIOR APPLICATION NUMBER: US 60/223,268
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: US 60/227,054
;  PRIOR FILING DATE: 2000-08-21
;  PRIOR APPLICATION NUMBER: US 60/231,121
;  PRIOR FILING DATE: 2000-09-08
;  PRIOR APPLICATION NUMBER: US 60/232,243
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;  PRIOR FILING DATE: 2000-09-13
;  PRIOR APPLICATION NUMBER: US 60/232,691
;  PRIOR FILING DATE: 2000-09-15
;  PRIOR APPLICATION NUMBER: US 60/235,146
;  PRIOR FILING DATE: 2000-09-22
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: PERL Program
; SEQ ID NO 1
;   LENGTH: 339
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US20040023252A1 7474806CD1
US-10-333-946-1

  Query Match            61.2%;  Score 1185;  DB 15;  Length 339;
  Best Local Similarity  99.6%;  Pred. No. 1.9e-104;
  Matches  225;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MLSILLPSRGSRSGSRRGALLLEGASRDMEKVDMNTSQEQGLCQFSEKYKQVYLSLAYSI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLSILLPSRGSRSGSRRGALLLEGASRDMEKVDMNTSQEQGLCQFSEKYKQVYLSLAYSI 60

Qy         61 IFILGLPLNGTVLWHSWGQTKRWSCATTYLVNLMVADLLYVLLPFLIITYSLDDRWPFGE 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 IFILGLPLNGTVLWHSWGQTKRWSCATTYLVNLMVADLLYVLLPFLIITYSLDDRWPFGE 120

Qy        121 LLCKLVHFLFYINLYGSILLLTCISVHQFLGVCHPLCSLPYRTRRHAWLGTSTTWALVVL 180
              ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        121 LLCKLVHFLFYINLYGSILLLTCISVHQFLGVWHPLCSLPYRTRRHAWLGTSTTWALVVL 180

Qy        181 QLLPTLAFSHTDYINGQMIWYDMTSQENFDRLFAYGIVLTLSGFLS 226
              |||||||||||||||||||||||||||||||||||||||||||||
Db        181 QLLPTLAFSHTDYINGQMIWYDMTSQENFDRLFAYGIVLTLSGFLS 226


RESULT 10
US-10-763-972-4
; Sequence 4, Application US/10763972
; Publication No. US20040137500A1
; GENERAL INFORMATION:
;  APPLICANT: PFIZER INC.
;  APPLICANT:  Fidock, Mark David
;  TITLE OF INVENTION: Novel Polypeptide
;  FILE REFERENCE: PC10960B
;  CURRENT APPLICATION NUMBER: US/10/763,972
;  CURRENT FILING DATE:  2004-01-23
;  PRIOR APPLICATION NUMBER: GB 0030855.1
;  PRIOR FILING DATE: 2000-12-18
;  PRIOR APPLICATION NUMBER: US 60/260,563
;  PRIOR FILING DATE: 2001-01-09
;  PRIOR APPLICATION NUMBER: US 60/265,688
;  PRIOR FILING DATE: 2001-02-01
;  PRIOR APPLICATION NUMBER: GB 0101222.8
;  PRIOR FILING DATE: 2001-01-17
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
;   LENGTH: 339
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-763-972-4

  Query Match            61.2%;  Score 1185;  DB 16;  Length 339;
  Best Local Similarity  99.6%;  Pred. No. 1.9e-104;
  Matches  225;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MLSILLPSRGSRSGSRRGALLLEGASRDMEKVDMNTSQEQGLCQFSEKYKQVYLSLAYSI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLSILLPSRGSRSGSRRGALLLEGASRDMEKVDMNTSQEQGLCQFSEKYKQVYLSLAYSI 60

Qy         61 IFILGLPLNGTVLWHSWGQTKRWSCATTYLVNLMVADLLYVLLPFLIITYSLDDRWPFGE 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 IFILGLPLNGTVLWHSWGQTKRWSCATTYLVNLMVADLLYVLLPFLIITYSLDDRWPFGE 120

Qy        121 LLCKLVHFLFYINLYGSILLLTCISVHQFLGVCHPLCSLPYRTRRHAWLGTSTTWALVVL 180
              ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        121 LLCKLVHFLFYINLYGSILLLTCISVHQFLGVWHPLCSLPYRTRRHAWLGTSTTWALVVL 180

Qy        181 QLLPTLAFSHTDYINGQMIWYDMTSQENFDRLFAYGIVLTLSGFLS 226
              |||||||||||||||||||||||||||||||||||||||||||||
Db        181 QLLPTLAFSHTDYINGQMIWYDMTSQENFDRLFAYGIVLTLSGFLS 226


RESULT 11
US-10-017-161-708
; Sequence 708, Application US/10017161
; Publication No. US20030143668A1
; GENERAL INFORMATION:
;  APPLICANT: SUWA, MAKIKO
;  APPLICANT:  ASAI, KIYOSHI
;  APPLICANT:  AKIYAMA, YUTAKA
;  APPLICANT:  ABURATANI, HIROYUKI
;  TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
;  FILE REFERENCE: 084335/0152
;  CURRENT APPLICATION NUMBER: US/10/017,161
;  CURRENT FILING DATE:  2002-12-18
;  PRIOR APPLICATION NUMBER: JP 2001/246789
;  PRIOR FILING DATE: 2001-06-18
;  NUMBER OF SEQ ID NOS: 2430
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 708
;   LENGTH: 271
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-017-161-708

  Query Match            48.7%;  Score 942;  DB 14;  Length 271;
  Best Local Similarity  86.5%;  Pred. No. 2.4e-81;
  Matches  179;  Conservative    6;  Mismatches   22;  Indels    0;  Gaps    0;

Qy         29 MEKVDMNTSQEQGLCQFSEKYKQVYLSLAYSIIFILGLPLNGTVLWHSWGQTKRWSCATT 88
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MEKVDMNTSQEQGLCQFSEKYKQVYLSLAYSIIFILGLPLNGTVLWHSWGQTKRWSCATT 60

Qy         89 YLVNLMVADLLYVLLPFLIITYSLDDRWPFGELLCKLVHFLFYINLYGSILLLTCISVHQ 148
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YLVNLMVADLLYVLLPFLIITYSLDDRWPFGELLCKLVHFLFYINLYGSILLLTCISVHQ 120

Qy        149 FLGVCHPLCSLPYRTRRHAWLGTSTTWALVVLQLLPTLAFSHTDYINGQMIWYDMTSQEN 208
              |||||||||||||||||||||||||||||||||||||||||||||||||||  : :||
Db        121 FLGVCHPLCSLPYRTRRHAWLGTSTTWALVVLQLLPTLAFSHTDYINGQMIWSLIKPEEN 180

Qy        209 FDRLFAYGIVLTLSGFLSLLGHFGVLF 235
                 |      ::   | : | | : |
Db        181 LMRTGNTARARSIRTILLVCGLFTLCF 207


RESULT 12
US-10-292-798-620
; Sequence 620, Application US/10292798
; Publication No. US20030235833A1
; GENERAL INFORMATION:
;  APPLICANT: SUWA, MAKIKO
;  APPLICANT:  ASAI, KIYOSHI
;  APPLICANT:  AKIYAMA, YUTAKA
;  APPLICANT:  ABURATANI, HIROYUKI
;  TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
;  FILE REFERENCE: 084335/166
;  CURRENT APPLICATION NUMBER: US/10/292,798
;  CURRENT FILING DATE:  2002-11-13
;  PRIOR APPLICATION NUMBER: 10/017,161
;  PRIOR FILING DATE: 2001-12-18
;  PRIOR APPLICATION NUMBER: JP 2001-246789
;  PRIOR FILING DATE: 2001-06-18
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;  NUMBER OF SEQ ID NOS: 2070
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 620
;   LENGTH: 271
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-292-798-620

  Query Match             48.7%;  Score 942;  DB 14;  Length 271;
  Best Local Similarity   86.5%;  Pred. No. 2.4e-81;
  Matches  179;  Conservative    6;  Mismatches   22;  Indels    0;  Gaps    0;

Qy          29 MEKVDMNTSQEQGLCQFSEKYKQVYLSLAYSIIFILGLPLNGTVLWHSWGQTKRWSCATT 88
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 MEKVDMNTSQEQGLCQFSEKYKQVYLSLAYSIIFILGLPLNGTVLWHSWGQTKRWSCATT 60

Qy          89 YLVNLMVADLLYVLLPFLIITYSLDDRWPFGELLCKLVHFLFYINLYGSILLLTCISVHQ 148
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 YLVNLMVADLLYVLLPFLIITYSLDDRWPFGELLCKLVHFLFYINLYGSILLLTCISVHQ 120

Qy         149 FLGVCHPLCSLPYRTRRHAWLGTSTTWALVVLQLLPTLAFSHTDYINGQMIWYDMTSQEN 208
               |||||||||||||||||||||||||||||||||||||||||||||||||||  :  :||
Db         121 FLGVCHPLCSLPYRTRRHAWLGTSTTWALVVLQLLPTLAFSHTDYINGQMIWSLIKPEEN 180

Qy         209 FDRLFAYGIVLTLSGFLSLLGHFGVLF 235
               |     ::   | : | | : |
Db         181 LMRTGNTARARSIRTILLVCGLFTLCF 207


RESULT 13
US-09-782-974C-14
; Sequence 14, Application US/09782974C
; Publication No. US20030082534A1
; GENERAL INFORMATION:
;  APPLICANT: Vogeli, Gabriel
;  APPLICANT:  Lind, Peter
;  APPLICANT:  Wood, Linda S.
;  APPLICANT:  Parodi, Luis A.
;  TITLE OF INVENTION: No. US20030082534A1el G Protein Coupled Receptor
;  FILE REFERENCE: 411USPHRM311
;  CURRENT APPLICATION NUMBER: US/09/782,974C
;  CURRENT FILING DATE:  2002-09-04
;  PRIOR APPLICATION NUMBER: 60/165,838
;  PRIOR FILING DATE: 1999-11-16
;  PRIOR APPLICATION NUMBER: 09/714,449
;  PRIOR FILING DATE: 2000-11-16
;  PRIOR APPLICATION NUMBER: 60/198,568
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: 60/166,071
;  PRIOR FILING DATE: 1999-11-17
;  PRIOR APPLICATION NUMBER: 60/166,678
;  PRIOR FILING DATE: 1999-11-19
;  PRIOR APPLICATION NUMBER: 60/173,396
;  PRIOR FILING DATE: 1999-12-28
;  PRIOR APPLICATION NUMBER: 60/184,129
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: 60/185,421
;  PRIOR FILING DATE: 2000-02-28
;  PRIOR APPLICATION NUMBER: 60/185,554
;  PRIOR FILING DATE: 2000-02-28
;  PRIOR APPLICATION NUMBER: 60/186,530
;  PRIOR FILING DATE: 2000-03-02
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 192
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
;   LENGTH: 170
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-782-974C-14

  Query Match             47.6%;  Score 921;  DB 10;  Length 170;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-79;
  Matches  170;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          83 WSCATTYLVNLMVADLLYVLLPFLIITYSLDDRWPFGELLCKLVHFLFYINLYGSILLLT 142
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 WSCATTYLVNLMVADLLYVLLPFLIITYSLDDRWPFGELLCKLVHFLFYINLYGSILLLT 60

Qy         143 CISVHQFLGVCHPLCSLPYRTRRHAWLGTSTTWALVVLQLLPTLAFSHTDYINGQMIWYD 202
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 CISVHQFLGVCHPLCSLPYRTRRHAWLGTSTTWALVVLQLLPTLAFSHTDYINGQMIWYD 120

Qy         203 MTSQENFDRLFAYGIVLTLSGFLSLLGHFGVLFTDGQEPDQARGEPHEDR 252
               ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 MTSQENFDRLFAYGIVLTLSGFLSLLGHFGVLFTDGQEPDQARGEPHEDR 170


RESULT 14
US-10-010-568-10
; Sequence 10, Application US/10010568
; Publication No. US20030157598A1
; GENERAL INFORMATION:
;  APPLICANT: Bristol-Myers Squibb Company
;  TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY23, EXPRESSED HIC
;  TITLE OF INVENTION:  KIDNEY
;  FILE REFERENCE: D0077 NP
;  CURRENT APPLICATION NUMBER: US/10/010,568
;  CURRENT FILING DATE:  2001-12-07
;  PRIOR APPLICATION NUMBER: US 60/251,926
;  PRIOR FILING DATE: 2000-12-07
;  PRIOR APPLICATION NUMBER: US 60/269,795
;  PRIOR FILING DATE: 2001-02-14
;  NUMBER OF SEQ ID NOS: 55
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
;   LENGTH: 328
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-10-010-568-10

  Query Match             23.1%;  Score 447;  DB 14;  Length 328;
  Best Local Similarity   45.9%;  Pred. No. 5.7e-34;
  Matches   85;  Conservative   31;  Mismatches   67;  Indels    2;  Gaps    2;

Qy          43 CQFSEKYKQVYLSLAYSIIFILGLPLNGTVLWHSWGQTKRWSCATTYLVNLMVADLLYVL 102
               | | |::||| | | ||::|:|||||  |:   |   |  :  | |::|| :||||||
Db          13 CTFHEEFKQVLLPLVYSVVFLLGLPLNAVVIGQIWLARKALTRTTIYMLNLAMADLLYVC 72

Qy         103 -LPFLIITYSLDDRWPFGELLCKLVHFLFYINLYGSILLLTCISVHQFLGVCHPLCSL-P 160
                || ||  |:  | ||||:  || | | || ||:|||| |||||| :::|:|||| |
Db          73 SLPLLIYNYTQKDYWPFGDFTCKFVRFQFYTNLHGSILFLTCISVQRYMGICHPLASWHK 132

Qy         161 YRTRRHAWLGTSTTWALVVLQLLPTLAFSHTDYINGQMIWYDMTSQENFDRLFAYGIVLT 220
               : ::  ||  :  | :|: | |||  |: |     : : ||::  :     | ||| ||
Db         133 KKGKKLTWLVCAAVWFIVIAQCLPTFVFASTGTQRNRTVCYDLSPPDRSTSYFPYGITLT 192

Qy         221 LSGFL 225
               ::|||
Db         193 ITGFL 197


RESULT 15
US-10-010-568-14
; Sequence 14, Application US/10010568
; Publication No. US20030157598A1
; GENERAL INFORMATION:
;  APPLICANT: Bristol-Myers Squibb Company
;  TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY23, EXPRESSED HIC
;  TITLE OF INVENTION:  KIDNEY
;  FILE REFERENCE: D0077 NP
;  CURRENT APPLICATION NUMBER: US/10/010,568
;  CURRENT FILING DATE:  2001-12-07
;  PRIOR APPLICATION NUMBER: US 60/251,926
;  PRIOR FILING DATE: 2000-12-07
;  PRIOR APPLICATION NUMBER: US 60/269,795
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;  PRIOR FILING DATE: 2001-02-14
;  NUMBER OF SEQ ID NOS: 55
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
;   LENGTH: 328
;   TYPE: PRT
;   ORGANISM: GALLUS GALLUS
US-10-010-568-14

  Query Match             23.1%;  Score 447;  DB 14;  Length 328;
  Best Local Similarity   45.9%;  Pred. No. 5.7e-34;
  Matches   85;  Conservative   31;  Mismatches   67;  Indels    2;  Gaps    2;

Qy         43 CQFSEKYKQVYLSLAYSIIFILGLPLNGTVLWHSWGQTKRWSCATTYLVNLMVADLLYVL 102
              | | |::||| | | ||::|:|||||  |:   |   |  :  | |::|| :||||||
Db         13 CTFHEEFKQVLLPLVYSVVFLLGLPLNAVVIGQIWLARKALTRTTIYMLNLAMADLLYVC 72

Qy        103 -LPFLIITYSLDDRWPFGELLCKLVHFLFYINLYGSILLLTCISVHQFLGVCHPLCSL-P 160
               || ||  |:  | ||||:  || | | || ||:|||| |||||| :::|:|||| |
Db         73 SLPLLIYNYTQKDYWPFGDFTCKFVRFQFYTNLHGSILFLTCISVQRYMGICHPLASWHK 132

Qy        161 YRTRRHAWLGTSTTWALVVLQLLPTLAFSHTDYINGQMIWYDMTSQENFDRLFAYGIVLT 220
              : ::  ||  :  | :|: | |||  |: |     : : ||::  :     | ||| ||
Db        133 KKGKKLTWLVCAAVWFIVIAQCLPTFVFASTGTQRNRTVCYDLSPPDRSTSYFPYGITLT 192

Qy        221 LSGFL 225
              ::|||
Db        193 ITGFL 197


Search completed: November  4, 2004, 17:04:28
Job time : 143 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 4, 2004, 16:43:39 ; Search time 40 Seconds
(without alignments)
865.951 Million cell updates/sec

Title: US-10-763-972-2
Perfect score: 1936
Sequence: 1 MLSILLPSRGSRSGSRRGAL.....QNKLGEHPAGRKRCPGLNRS 360

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	400	20.7	328	2	I55450	G protein-coupled
2	387.5	20.0	328	2	JC4800	P2Y6 receptor - hu
3	374.5	19.3	375	2	A54946	P-2U nucleotide re
4	371	19.2	373	2	A47556	ATP receptor P2u -
5	367	19.0	365	2	S68679	G protein-coupled
6	346	17.9	362	2	S33733	G protein-coupled
7	328	16.9	373	2	JC4737	G protein-coupled
8	326.5	16.9	373	2	JC4162	P2Y receptor - bov
9	282.5	14.6	308	2	I50241	G protein-coupled
10	274.5	14.2	344	2	T09508	intron 17 purinerg
11	258.5	13.4	370	2	JC5549	heptahelical P2Y5-
12	258	13.3	353	2	JC2492	G protein-coupled
13	248.5	12.8	391	2	A41795	somatostatin recep
14	247.5	12.8	359	2	S15403	angiotensin II rec
15	246	12.7	399	2	I48705	proteinase activat
16	245.5	12.7	391	2	A39297	somatostatin recep
17	244.5	12.6	359	2	S44425	angiotensin II rec
18	244.5	12.6	391	2	C41795	somatostatin recep
19	242.5	12.5	397	2	S66518	proteinase-activat
20	242	12.5	359	2	JC1104	angiotensin II rec
21	241.5	12.5	420	2	I51667	thrombin receptor
22	239	12.3	359	2	I39418	angiotensin II rec
23	238	12.3	359	2	A48857	angiotensin II rec
24	237.5	12.3	359	2	A42656	angiotensin II rec
25	237	12.2	359	2	JH0621	angiotensin II rec
26	237	12.2	359	2	JC2134	angiotensin II rec
27	234.5	12.1	354	2	I53033	G protein-coupled
28	234.5	12.1	362	2	S68207	G protein-coupled
29	234.5	12.1	362	2	A57641	G protein-coupled
30	231.5	12.0	423	2	JC7677	allatostatin recep
31	230.5	11.9	359	2	JC1194	angiotensin II rec
32	230.5	11.9	362	2	B57641	G protein-coupled
33	230	11.9	352	1	S27357	complement C5a ana
34	229	11.8	360	2	JC4587	chemokine (C-C) re
35	227	11.7	371	2	JC5498	G protein-coupled
36	226.5	11.7	359	2	JQ1516	angiotensin II rec
37	226.5	11.7	425	2	A37912	thrombin receptor
38	225.5	11.6	372	2	S26667	G protein-coupled
39	224.5	11.6	380	2	I38435	angiotensin recept
40	223	11.5	365	2	S68208	G protein-coupled
41	221	11.4	371	2	JC5796	probable chemoattr
42	221	11.4	398	2	I56504	mu opioid receptor
43	220.5	11.4	351	2	B42009	FMLP-related recep
44	220	11.4	398	2	A57510	mu opioid receptor
45	220	11.4	398	2	I56517	mu opioid receptor

ALIGNMENTS

RESULT 1
I55450
G protein-coupled P2 receptor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I55450
R;Chang, K.; Hanaoka, K.; Kumada, M.; Takuwa, Y.
J. Biol. Chem. 270, 26152-26158, 1995
A;Title: Molecular cloning and functional analysis of a novel P2 nucleotide receptor.
A;Reference number: I55450; MUID:96064682; PMID:7592819.
A;Accession: I55450
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-328 <RES>
A;Cross-references: UNIPROT:Q63371; GB:D63665; NID:g1066007; PIDN:BAA09816.1; PID:g106600
C;Superfamily: ATP receptor P2u
C;Keywords: G protein-coupled receptor

Query Match 20.7%; Score 400; DB 2; Length 328;
Best Local Similarity 32.5%; Pred. No. 2.3e-27;
Matches 108; Conservative 53; Mismatches 137; Indels 34; Gaps 9;

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Qy          29 MEKVDMNTSQEQGL----CQFSEKYKQVYLSLAYSIIFILGLPLNGTVLWHSWGQTKRWS 84
               ||: |  | |  ||    | : | :|:: |   ||:: ::||||  |:      : :
Db           1 MER-DNGTIQAPGLPPTTCVYREDFKRLLLPPVYSVVLVVGLPLNVCVIAQICASRRTLT 59

Qy          85 CATTYLVNLMVADLLYVL-LPFLIITYSLDDRWPFGELLCKLVHFLFYINLYGSILLLTC 143
                 :  | :|| :|||||   || ||  |:  | ||||:| |:|| |||| ||:|||| |||
Db          60 RSAVYTLNLALADLLYACSLPLLIYNYARGDHWPFGDLACRLVRFLFYANLHGSILFLTC 119

Qy         144 ISVHQFLGVCHPLCSLPYR-TRRHAWLGTSTTWALVVLQLLPTLAFSHTDYINGQMIWYD 202
               ||  ::||:|||      |  || ||:     | :|  | |||  |: |     : : ||
Db         120 ISFQRYLGICHPLAPWHKRGGRRAAWVVCGVVWLVVTAQCLPTAVFAATGIQRNRTVCYD 179

Qy         203 MTSQENFDRLFAYGIVLTLSGFL----SLLGHFGVLFTDGQEPDQARGEPHEDRQHSPSQ 258
               ::       |   ||: ||: |||    :|| :  :       |   |   ::|:   ::
Db         180 LSPPILSTRYLPYGMALTVIGFLLPFTALLACYCRMARRLCRQDGPAGPVAQERRSKAAR 239

Qy         259 VHPDHPTGVWPLHPLFCALPYHSLLLPHHLL-SAFSGLPALDGSQCGLQDMEASGECEQL 317
               :            :  |  :    || |:  :|:  : :  |  | : :  |:
Db         240 M------------AVVVAAVFVISFLPFHITKTAYLAVRSTPGVSCPVLETFAAAYKGTR 287

Qy         318 PQPS------PVLSF----KGGKNRVRLLQKL 339
               |  |       |:| :    |  :    |||||
Db         288 PFASANSVLDPILFYFTQQKFRRQPHDLLQKL 319
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RESULT 2
JC4800
P2Y6 receptor - human
C;Species: Homo sapiens (man)
C;Date: 15-Oct-1995 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004

```
C;Accession: JC4800; G02514
R;Communi, D.; Parmentier, M.; Boeynaems, J.M.
Biochem. Biophys. Res. Commun. 222, 303-308, 1996
A;Title: Cloning, functional expression and tissue distribution of the human P2Y6 recept
A;Reference number: JC4800; MUID:96222498; PMID:8670200
A;Accession: JC4800
A;Molecule type: mRNA
A;Residues: 1-328 <COM>
A;Cross-references: UNIPROT:Q15077; EMBL:X97058
A;Experimental source: placenta
R;Hammet, F.; Southey, M.C.; Somers, G.R.; Hutchins, A.M.; Venter, D.J.
submitted to the EMBL Data Library, March 1996
A;Reference number: H01373
A;Accession: G02514
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 'M',4-328 <HAM>
A;Cross-references: EMBL:U52464; NID:g1407632; PIDN:AAB03572.1; PID:g1407633
C;Genetics:
A;Gene: P2Y6
C;Superfamily: ATP receptor P2u
C;Keywords: glycoprotein; placenta; receptor; transmembrane protein
F;26-52/Domain: transmembrane #status predicted <TMM1>
F;63-86/Domain: transmembrane #status predicted <TMM2>
F;104-122/Domain: transmembrane #status predicted <TMM3>
F;143-167/Domain: transmembrane #status predicted <TMM4>
F;193-216/Domain: transmembrane #status predicted <TMM5>
F;241-264/Domain: transmembrane #status predicted <TMM6>
F;283-305/Domain: transmembrane #status predicted <TMM7>
F;5,173/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             20.0%;  Score 387.5;  DB 2;  Length 328;
  Best Local Similarity   32.7%;  Pred. No. 2.8e-26;
  Matches  108;  Conservative   42;  Mismatches  143;  Indels   37;  Gaps    9;

Qy         33 DMNTSQEQGL----CQFSEKYKQVYLSLAYSIIFILGLPLNGTVLWHSWGQTKRWSCATT 88
              |  | |  ||     | : | :||: |    || :   |||||  |:       :  :
Db          4 DNGTGQALGLPPTTCVYRENFKQLLLPPVYSAVLAAGLPLNICVITQICTSRRALTRTAV 63

Qy         89 YLVNLMVADLLYVL-LPFLIITYSLDDRWPFGELLCKLVHFLFYINLYGSILLLTCISVH 147
              | :|| :|||||   || ||  |:  | ||||:  |:|| |||| ||:|||| |||||
Db         64 YTLNLALADLLYACSLPLLIYNYAQGDHWPFGDFACRLVRFLFYANLHGSILFLTCISFQ 123

Qy        148 QFLGVCHPLCSLPYR-TRRHAWLGTSTTWALVVLQLLPTLAFSHTDYINGQMIWYDMTSQ 206
             ::||:||||     |  || |||     |  |  | |||  |: |     : : ||::
Db        124 RYLGICHPLAPWHKRGGRRAAWLVCVAVWLAVTTQCLPTAIFAATGIQRNRTVCYDLSPP 183

Qy        207 ENFDRLFAYGIVLTLSGFL----SLLGHFGVLFTDGQEPDQARGEPHEDRQHSPSQVHPD 262
                ||: ||: |||    :||  : :|                ||  |::
Db        184 ALATHYMPYGMALTVIGFLLPFAALLACYCLLAC-----------RLCRQDGPAEPVAQ 231

Qy        263 HPTGVWPLHPLFCALPYHSLLLPHHLL-SAFSGLPALDGSQCGLQDMEASGECEQLPQP- 320
                 |      :  |  :    || |:  :|:  : :  |  | :  :||     :  :|
Db        232 ERRGKAARMAVVVAAAFAISFLPFHITKTAYLAVRSTPGVPCTV--LEAFAAAYKGTRPF 289

Qy        321 -------SPVLSF----KGGKNRVRLLQKL 339
                    |:| :    |  :    |||||
Db        290 ASANSVLDPILFYFTQKKFRRRPHELLQKL 319


RESULT 3
A54946
P-2U nucleotide receptor - human
C;Species: Homo sapiens (man)
C;Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 17-Mar-1999
C;Accession: A54946
R;Parr, C.E.; Sullivan, D.M.; Paradiso, A.M.; Lazarowski, E.R.; Burch, L.H.; Olsen, J.C.
Proc. Natl. Acad. Sci. U.S.A. 91, 3275-3279, 1994
A;Title: Cloning and expression of a human P-2U nucleotide receptor, a target for cystic
A;Reference number: A54946; MUID:94211846; PMID:8159738
A;Accession: A54946
A;Status: preliminary
A;Molecule type: mRNA; protein
A;Residues: 1-375 <PAR>
A;Cross-references: GB:U07225
A;Note: parts of this sequence were confirmed by protein sequencing
C;Genetics:
A;Gene: GDB:P2RY2; HP2U; P2U
A;Cross-references: GDB:362713; OMIM:600041
A;Map position: 11q13.5-11q14.1
C;Superfamily: ATP receptor P2u
C;Keywords: G protein-coupled receptor; transmembrane protein

  Query Match             19.3%;  Score 374.5;  DB 2;  Length 375;
  Best Local Similarity   32.7%;  Pred. No. 4.5e-25;
  Matches  115;  Conservative   43;  Mismatches  123;  Indels   71;  Gaps   13;

Qy         43 CQFSEKYKQVYLSLAYSIIFILGLPLNGTVLWHSWGQTKRWSCATTYLVNLMVADLLYVL 102
              |:|:| :| | | ::| :: :||| ||    |:     : | |: :|||: :| |:| ||
Db         25 CRFNEDFKYVLLPVSYGVVCVLGLCLNAVGLYIFLCRLKTWNASTTYMFHLAVSDALYAA 84

Qy        103 -LPFLIITYSLDDRWPFGELLCKLVHFLFYINLYGSILLLTCISVHQFLGVCHPLCSLPY 161
               || |:  |:  | |||  :||||| |||| ||| ||| ||||||: |||  || || :
Db         85 SLPLLVYYYARGDHWPFSTVLCKLVRFLFYTNLYCSILFLTCISVHRCLGVLRPLRSLRW 144

Qy        162 RTRRHAWLGTSTTWALVVLQLLPTLAFSHTDYINGQMIWYDMTSQENFDRLFAYGIVLTL 221
                |:|       | ||:    | | |  |    | :  :| :: | | |  ||  |:
Db        145 GRARYARRVAGAVWVLVLACQAPVLYFVTTS-ARGPLTCHDTSAPELFSRFVAYSSVM-- 201

Qy        222 SGFLSLLGHFGVLF-------------------TDGQEPDQARGEPHEDRQHSPSQVHP 261
                | ||  | | |                     | |       | |   |:   :
Db        202 ---LGLL--FAVPFAVILVCYVLMARRLLKPAYGTSG-------GLPRAKRKSVRT---- 245

Qy        262 DHPTGVWPLHPLF--CALPYH----------SLLLPHHLLSAFSGLPALDGSQCGLQDME 309
                :  :  :|  | ||:|          || |  | |:| :           :  :
Db        246 -----IAVVLAVFALCFLPFHVTRTLYYSFRSLDLSCHTLNAIN-------MAYKVTRLA 293

Qy        310 ASGECEQLPQPSPVLSFKGGKNRVRLLQKLRQNKLGEHPA-GRKRCPGLNRS 360
              ::  |       ||| |  |:  ||  :  :    |  ||   :|  || ||
Db        294 SANSC-----LDPVLYFLAGQRLVRFARDAKP-PTGPSPATPARRTLGLRRS 339


RESULT 4
A47556
ATP receptor P2u - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: A47556
R;Lustig, K.D.; Shiau, A.K.; Brake, A.J.; Julius, D.
Proc. Natl. Acad. Sci. U.S.A. 90, 5113-5117, 1993
A;Title: Expression cloning of an ATP receptor from mouse neuroblastoma cells.
A;Reference number: A47556; MUID:93281707; PMID:7685114
A;Accession: A47556
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-373 <LUS>
A;Cross-references: UNIPROT:P35383; GB:L14751; NID:g309457; PIDN:AAA39871.1; PID:g309458
C;Superfamily: ATP receptor P2u
C;Keywords: transmembrane protein

  Query Match             19.2%;  Score 371;  DB 2;  Length 373;
  Best Local Similarity   31.6%;  Pred. No. 9.1e-25;
  Matches  113;  Conservative   42;  Mismatches  115;  Indels   88;  Gaps   12;

Qy         43 CQFSEKYKQVYLSLAYSIIFILGLPLNGTVLWHSWGQTKRWSCATTYLVNLMVADLLYVL 102
              |:|:| :| | | ::| :: :||| ||    |:     : | |: :|||: :| |:| ||
Db         25 CRFNEDFKYVLLPVSYGVVCVLGLCLNVVALYIFLCRLKTWNASTTYMFHLAVSDSLYAA 84

Qy        103 -LPFLIITYSLDDRWPFGELLCKLVHFLFYINLYGSILLLTCISVHQFLGVCHPLCSLPY 161
               || |:  |:  | |||  :||||| |||| ||| ||| |||||||: |||  || || :
Db         85 SLPLLVYYYARGDHWPFSTVLCKLVRFLFYTNLYCSILFLTCISVHRCLGVLRPLHSLRW 144

Qy        162 RTRRHAWLGTSTTWALVVLQLLPTLAFSHTDYINGQMIWYDMTSQENFDRLFAYGIVLTL 221
                |:|     :  | ||:    | | |  |      ::  :| :::| | |    ||  |:
Db        145 GRARYARRVAAVVWVLVLACQAPVLYFVTTSVRGTRITCHDTSARELFSHFVAYSSVM-- 202
```

```
Qy        222 SGFLSLLGHFGVLF--------------------TDGQEPDQARGEPHEDRQ--HSPSQV 259
Db        203 ---LGLL--FAVPFSVILVCYVLMARRLLKPAYGTTG-------GLPRAKRKSVRTIALV 250

Qy        260 HPDHPTGVWPLHPLFCALPYH----------SLLLPHHLLSAFS-----GLPALDGSQCG 304
Db        251 -----LAVFAL----CFLPFHVTRTLYYSFRSLDLSCHTLNAINMAYKITRPLASANSC- 300

Qy        305 LQDMEASGECEQLPQPSPVLSFKGGKNRVRLLQKLR-----------QNKLGEHPAGR 351
Db        301 --------------LDPVLYFLAGQRLVRFARDAKPPTEPTPSPQARRKLGLHRPNR 343


RESULT 5
S68679
G protein-coupled receptor - human
C;Species: Homo sapiens (man)
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S68679
R;Stam, N.J.; Klomp, J.; van de Heuvel, M.; Olijve, W.
FEBS Lett. 384, 260-264, 1996
A;Title: Molecular cloning and characterization of a novel orphan receptor (P(2P)) expre
A;Reference number: S68679; MUID:96197801; PMID:8617367
A;Accession: S68679
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-365 <STA>
A;Cross-references: UNIPROT:P51582; EMBL:X96597; NID:g1296631; PIDN:CAA65415.1; PID:g129
C;Superfamily: ATP receptor P2u
C;Keywords: G protein-coupled receptor

  Query Match             19.0%;  Score 367;  DB 2;  Length 365;
  Best Local Similarity   41.1%;  Pred. No. 2e-24;
  Matches   79;  Conservative   30;  Mismatches   75;  Indels    8;  Gaps    3;

Qy         43 CQFSEKYKQVYLSLAYSIIFILGLPLNGTVLWHSWGQTKRWSCATTYLVNLMVADLLYVL 102
Db         27 CWFDEDFKFILLPVSYAVVFVLGLGLNAPTLWLFIFRLRPWDATATYMFHLALSDTLYVL 86

Qy        103 -LPFLIITYSLDDRWPFGELLCKLVHFLFYINLYGSILLLTCISVHQFLGVCHPLCSLPY 161
Db         87 SLPTLIYYYAAHNHWPFGTEICKFVRFLFYWNLYCSVLFLTCISVHRYLGICHPLRALRW 146

Qy        162 RTRRHAWLGTSTTWALVVLQLLPTLAFSHTDYINGQMIWYDMTSQENFDRLFAYGIVLTL 221
Db        147 GRPRLAGLLCLAVWLVVAGCLVPNLFFVTTSNKGTTVLCHDTTRPEEFDHYVHFS----- 201

Qy        222 SGFLSLLGHFGV 233
Db        202 SAVMGLL--FGV 211


RESULT 6
S33733
G protein-coupled receptor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: S33733
R;Webb, T.E.; Simon, J.; Krishek, B.J.; Bateson, A.N.; Smart, T.G.; King, B.F.; Burnstoc
FEBS Lett. 324, 219-225, 1993
A;Title: Cloning and functional expression of a brain G-protein-coupled ATP receptor.
A;Reference number: S33733; MUID:93285340; PMID:8508924
A;Accession: S33733
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-362 <WEB>
A;Cross-references: UNIPROT:P34996; EMBL:X73268; NID:g395084; PIDN:CAA51716.1; PID:g3950
C;Superfamily: ATP receptor P2u
C;Keywords: G protein-coupled receptor; transmembrane protein

  Query Match             17.9%;  Score 346;  DB 2;  Length 362;
  Best Local Similarity   30.5%;  Pred. No. 1.4e-22;
  Matches   97;  Conservative   49;  Mismatches  128;  Indels   44;  Gaps   10;

Qy         53 YLSLAYSIIFILGLPLNGTVLWHSWGQTKRWSCATTYLVNLMVADLLYVL-LPFLIITYS 111
Db         42 YLPTVYILVFITGFLGNSVAIWMFVFHMRPWSGISVYMFNLALADFLYVLTLPALIFYYF 101

Qy        112 LDDRWPFGELLCKLVHFLFYINLYGSILLLTCISVHQFLGVCHPLCSLPYRTRRHAWLGT 171
Db        102 NKTDWIFGDVMCKLQRFIFHVNLYGSILFLTCISVHRYTGVVHPLKSLGRLKKKNAVYVS 161

Qy        172 STTWALVVLQLLPTLAFSHTDYINGQMI-WYDMTSQENFDRLFAYGIVLTL----SGFLS 226
Db        162 SLVWALVVAVIAPILFYSGTGVRRNKTITCYDTTADEYLRSYFVYSMCTTVFMFCIPFIV 221

Qy        227 LLGHFGVLFTDGQEPDQARGEPHEDRQHSPSQVHPDHPTGVWPLHPLFCALPYHSL-LLP 285
Db        222 ILGCYGLI---------VKALIYKDLDNSPLRRK--------SIYLVIIVLTVFAVSYLP 264

Qy        286 HHLLSAFSGLPALD---GSQCGLQD-----------MEASGECEQLPQPSPVLSFKGGKN 331
Db        265 FHVMKTLNLRARLDFQTPQMCAFNDKVYATYQVTRGLASLNSC-----VDPILYFLAGDT 319

Qy        332 -RVRLLQKLRQNKLGEHP 348
Db        320 FRRRLLSRATRKSSRRSEP 337


RESULT 7
JC4737
G protein-coupled receptor P2Y1 - human
N;Alternate names: P2Y1 purinergic receptor; P2Y1 purinoceptor
C;Species: Homo sapiens (man)
C;Date: 10-May-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C;Accession: JC4737; JC4615; S54253
R;Janssens, R.; Communi, D.; Pirotton, S.; Samson, M.; Parmentier, M.; Boeynaems, J.M.
Biochem. Biophys. Res. Commun. 221, 588-593, 1996
A;Title: Cloning and tissue distribution of the human P2Y1 receptor.
A;Reference number: JC4737; MUID:96205320; PMID:8630005
A;Accession: JC4737
A;Molecule type: DNA
A;Residues: 1-373 <JAN>
A;Cross-references: UNIPROT:P47900; GB:S81950; NID:g1839438; PIDN:AAB47091.1; PID:g183941
R;Ayyanathan, K.; Webbs, T.E.; Sandhu, A.K.; Athwal, R.S.; Barnard, E.A.; Kunapuli, S.P.
Biochem. Biophys. Commun. 218, 783-788, 1996
A;Title: Cloning and chromosomal localization of the human P2Y1 purinoceptor.
A;Reference number: JC4615; MUID:96158962; PMID:8579591
A;Accession: JC4615
A;Molecule type: mRNA
A;Residues: 1-373 <AYY>
A;Cross-references: GB:U42029; NID:g1147730; PIDN:AAA97872.1; PID:g1147731
A;Experimental source: erythro leukemia cells
R;Leon, C.; Vial, C.; Cazenave, J.; Gachet, C.
submitted to the EMBL Data Library, May 1995
A;Description: Cloning of a human putative P2Y receptor.
A;Reference number: S54253
A;Accession: S54253
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-137,139-373 <LEO>
A;Cross-references: EMBL:Z49205; NID:g798835; PIDN:CAA89066.1; PID:g798836
C;Comment: This receptor belongs to a family of G protein-coupled receptors. It responds
C;Genetics:
A;Gene: p2Y1; GDB:P2RY1
A;Cross-references: GDB:677125; OMIM:601167
A;Map position: 3pter-3qter
C;Superfamily: ATP receptor P2u
C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prote
F;52-77/Domain: transmembrane #status predicted <TM1>
F;88-111/Domain: transmembrane #status predicted <TM2>
F;124-152/Domain: transmembrane #status predicted <TM3>
F;171-191/Domain: transmembrane #status predicted <TM4>
F;214-237/Domain: transmembrane #status predicted <TM5>
F;261-282/Domain: transmembrane #status predicted <TM6>
F;305-328/Domain: transmembrane #status predicted <TM7>
```

```
F;11,27,113,197/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;258,336/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predict
F;330,339/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predict
F;343/Binding site: phosphate (Ser) (covalent) (by protein kinase C and calmodulin-depen

  Query Match             16.9%;  Score 328;  DB 2;  Length 373;
  Best Local Similarity   29.9%;  Pred. No. 5.3e-21;
  Matches   93;  Conservative   51;  Mismatches  123;  Indels   44;  Gaps   10;

Qy          53 YLSLAYSIIFILGLPLNGTVLWHSWGQTKRWSCATTYLVNLMVADLLYVL-LPFLIITYS 111
               ||    | ::||:|    |   :|      | ||  : |: || :|| |||| || ||  |
Db          53 YLPAVYILVFIIGFLGNSVAIWMFVFHMKPWSGISVYMFNLALADFLYVLTLPALIFYYF 112

Qy         112 LDDRWPFGELLCKLVHFLFYINLYGSILLLTCISVHQFLGVCHPLCSLPYRTRRHAWLGT 171
                 | ||: :|||  |:|::||||||| ||||| |:: || :|| ||    :::|   :
Db         113 NKTDWIFGDAMCKLQRFIFHVNLYGSILFLTCISAHRYSGVVYPLKSLGRLKKKNAICIS 172

Qy         172 STTWALVVLQLLPTLAFSHTDYINGQMI-WYDMTSQENFDRLFAYGIVLTLSGF----LS 226
                 | :||: : | | :| |     : |  || || |     | | :  |:: |    :
Db         173 VLVWLIVVVAISPILFYSGTGVRKNKTITCYDTTSDEYLRSYFIYSMCTTVAMFCVPLVL 232

Qy         227 LLGHFGVLFTDGQEPDQARGEPHEDRQHSPSQVHPDHPTGVWPLHPLFCALPYHSL-LLP 285
               :|| :|::              |   ::|  :|| :             :: :   |   ::  :|
Db         233 ILGCYGLI---------VRALIYKDLDNSPLRRK--------SIYLVIIVLTVFAVSYIP 275

Qy         286 HHLLSAFSGLPALD---GSQCGLQD----------MEASGECEQLPQPSPVLSFKGGKN 331
               |::   :    ||   : |   |             : :   |       |:| |  |
Db         276 FHVMKTMNLRARLDFQTPAMCAFNDRVYATYQVTRGLASLNSC-----VDPILYFLAGDT 330

Qy         332 -RVRLLQKLRQ 341
                | ||  :  |:
Db         331 FRRRLSRATRK 341


RESULT 8
JC4162
P2Y receptor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 12-Oct-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: JC4162
R;Henderson, D.J.; Elliot, D.G.; Smith, G.M.; Webb, T.E.; Dainty, I.A.
Biochem. Biophys. Res. Commun. 212, 648-656, 1995
A;Title: Cloning and characterisation of a bovine P2Y receptor.
A;Reference number: JC4162; MUID:95352058; PMID:7626079
A;Accession: JC4162
A;Molecule type: mRNA
A;Residues: 1-373 <HEN>
A;Cross-references: UNIPROT:P48042; EMBL:X87628; NID:g1032484; PIDN:CAA60958.1; PID:g103
A;Experimental source: aortic endothelial cell
C;Genetics:
A;Gene: bovp2y
C;Superfamily: ATP receptor P2u
C;Keywords: glycoprotein; phosphoprotein; receptor; transmembrane protein
F;52-77/Domain: transmembrane #status predicted <TM1>
F;88-111/Domain: transmembrane #status predicted <TM2>
F;124-150/Domain: transmembrane #status predicted <TM3>
F;171-191/Domain: transmembrane #status predicted <TM4>
F;214-237/Domain: transmembrane #status predicted <TM5>
F;261-282/Domain: transmembrane #status predicted <TM6>
F;305-328/Domain: transmembrane #status predicted <TM7>
F;11,27,113,197/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;258/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted

  Query Match             16.9%;  Score 326.5;  DB 2;  Length 373;
  Best Local Similarity   36.7%;  Pred. No. 7.2e-21;
  Matches   77;  Conservative   35;  Mismatches   83;  Indels   15;  Gaps    4;

Qy          53 YLSLAYSIIFILGLPLNGTVLWHSWGQTKRWSCATTYLVNLMVADLLYVL-LPFLIITYS 111
               ||    | ::||:|    |   :|      | ||  : |: || :|| |||| || ||  |
Db          53 YLPAVYILVFIIGFLGNSVAIWMFVFHMKPWSGISVYMFNLALADFLYVLTLPALIFYYF 112

Qy         112 LDDRWPFGELLCKLVHFLFYINLYGSILLLTCISVHQFLGVCHPLCSLPYRTRRHAWLGT 171
                 | ||: :|||  |:|::||||||| ||||| |:: || :|| ||    :::|   :

Db         113 NKTDWIFGDAMCKLQRFIFHVNLYGSILFLTCISAHRYSGVVYPLKSLGRLKKKNAVYIS 172

Qy         172 STTWALVVLQLLPTLAFSHTDYINGQMI-WYDMTSQENFDRLFAYGIVLTLSGF----LS 226
                 | :||: : | | :| |     : |  || || |     | | :  |:: |    :
Db         173 VLVWLIVVVGISPILFYSGTGIRKNKTITCYDTTSDEYLRSYFIYSMCTTVAMFCVPLVL 232

Qy         227 LLGHFGVLFTDGQEPDQARGEPHEDRQHSP 256
               :|| :|::           |   ::|  :||
Db         233 ILGCYGLI---------VRALIYKDLDNSP 253


RESULT 9
I50241
G protein-coupled receptor 6H1 - chicken
N;Alternate names: purinoceptor 6H1
C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: I50241; JC4618
R;Kaplan, M.H.; Smith, D.I.; Sundick, R.S.
J. Immunol. 151, 628-636, 1993
A;Title: Identification of a G protein coupled receptor induced in activated T cells.
A;Reference number: I50241; MUID:93329058; PMID:8393036
A;Accession: I50241
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-308 <KAP>
A;Cross-references: UNIPROT:P32250; GB:L06109; NID:g304383; PIDN:AAB06587.1; PID:g304384
R;Webb, T.E.; Kaplan, M.G.; Barnard, E.A.
Biochem. Biophys. Res. Commun. 219, 105-110, 1996
A;Title: Identification of 6H1 as a P2Y purinoceptor: P2Y5.
A;Reference number: JC4618; MUID:96190677; PMID:8619790
A;Accession: JC4618
A;Molecule type: mRNA
A;Residues: 1-308 <WEB>
A;Cross-references: GB:L06109; NID:g304383; PIDN:AAB06587.1; PID:g304384
A;Experimental source: T-cells
C;Comment: This receptor plays a role in T-cell activation.
C;Genetics:
A;Gene: p2Y5
C;Superfamily: ATP receptor P2u
C;Keywords: G protein-coupled receptor; transmembrane protein
F;15-40/Domain: transmembrane #status predicted <TM1>
F;51-74/Domain: transmembrane #status predicted <TM2>
F;89-109/Domain: transmembrane #status predicted <TM3>
F;133-153/Domain: transmembrane #status predicted <TM4>
F;177-201/Domain: transmembrane #status predicted <TM5>
F;227-248/Domain: transmembrane #status predicted <TM6>
F;269-292/Domain: transmembrane #status predicted <TM7>

  Query Match             14.6%;  Score 282.5;  DB 2;  Length 308;
  Best Local Similarity   36.1%;  Pred. No. 4.1e-17;
  Matches   70;  Conservative   31;  Mismatches   80;  Indels   13;  Gaps    5;

Qy          43 CQFSEKYKQVYLSLAYSIIFILGLPLNGTVLWHSWGQTKRWSCATTYLVNLMVADLLYVL 102
               |   : :|       :|::|:|||  |   ::      |  :  |||::|| ::|||:|
Db           6 CSTEDSFKYTLYGCVFSMVFVLGLIANCVAIYIFTFTLKVRNETTTYMLNLAISDLLFVF 65

Qy         103 -LPFLIITYSLDDRWPFGELLCKLVHFLFYINLYGSILLLTCISVHQFLGVCHPLCSLPY 161
                |||  |  | :   ||||::|||:   ||| |:|||| |||||| :|| : ||  |
Db          66 TLPFRIY-YFVVRNWPFGDVLCKISVTLFYTNMYGSILFLTCISVDRFLAIVHPFRSKTL 124

Qy         162 RTRRHAWLGTSTTWALVVLQLLPTLAFSHTDYINGQMIWYDMTSQENFD----RLFAYGI 217
               ||:|:| :     |  |:    |  |  |  | |      | |||     : :   |
Db         125 RTKRNARIVCVAVWITVLAGSTPASFFQST---NRQNNTEQRTCFENFPPESTWKTYLSRI 181

Qy         218 VLTLSGFLSLLGHF 231
               |:    |: ::| |
Db         182 VI----FIEIVGFF 191


RESULT 10
T09508
intron 17 purinergic receptor P2Y5 - human
```

```
N;Alternate names: G-protein coupled receptor
C;Species: Homo sapiens (man)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T09508
R;Bohm, S.K.; Trumpp, A.; Khitin, L.M.; Kong, W.; Payan, D.G.; Bunnett, N.W.
submitted to the EMBL Data Library, April 1997
A;Description: The human purinergic receptor P2Y5 is encoded in intron 17 of the retinob
A;Reference number: Z16705
A;Accession: T09508
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-344 <BOH>
A;Cross-references: UNIPROT:P43657; EMBL:AF000546; NID:g2232068; PID:g2232069
C;Genetics:
A;Map position: 13
C;Superfamily: ATP receptor P2u
C;Keywords: G protein-coupled receptor; transmembrane protein

  Query Match             14.2%;  Score 274.5;  DB 2;  Length 344;
  Best Local Similarity   33.8%;  Pred. No. 2.4e-16;
  Matches   70;  Conservative   39;  Mismatches   77;  Indels   21;  Gaps    7;

Qy         32 VDMNTSQEQGLCQFSEKYKQVYLSLAYSIIFILGLPLNGTVLWHSWGQTKRWSCATTYLV 91
              | :|:|      | ::: :|        :|::|:|||  |   ::       |  :  |||::
Db          2 VSVNSSH----CFYNDSFKYTLYGCMFSMVFVLGLVSNCVAIYIFICVLKVRNETTTYMI 57

Qy         92 NLMVADLLYVL-LPFLIITYSLDDRWPFGELLCKLVHFLFYINLYGSILLLTCISVHQFL 150
              || ::|||:|  |||  |  |     ||||:||||:   ||| |:|||| |||||| :||
Db         58 NLAMSDLLFVFTLPFRIF-YFTTRNWPFGDLLCKISVMLFYTNMYGSILFLTCISVDRFL 116

Qy        151 GVCHPLCSLPYRTRRHAWLGTSTTWALVVLQLLPT--LAFSHTDYINGQMIWYDMTSQEN 208
               : :|  |   ||:|:|  :  :  |  |:    |   :  :|:  |     :     ||
Db        117 AIVYPFKSKTLRTKRNAKIVCTGVWLTVIGGSAPAVFVQSTHSQGNNASEACF-----EN 171

Qy        209 FD----RLFAYGIVLTLSGFLSLLGHF 231
              |     : :   ||:    |: ::| |
Db        172 FPEATWKTYLSRIVI----FIEIVGFF 194


RESULT 11
JC5549
heptahelical P2Y5-like receptor - human
C;Species: Homo sapiens (man)
C;Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 09-Jul-2004
C;Accession: JC5549
R;Janssens, R.; Boeynaems, J.M.; Godart, M.; Communi, D.
Biochem. Biophys. Res. Commun. 236, 106-112, 1997
A;Title: Cloning of a human heptahelical receptor closely related to the P2Y5 receptor.
A;Reference number: JC5549; MUID:97366605; PMID:9223435
A;Accession: JC5549
A;Molecule type: DNA
A;Residues: 1-370 <JAN>
A;Cross-references: UNIPROT:Q99677; DDBJ:AF005419; NID:g2240034; PIDN:AAB66322.1; PID:g2
C;Superfamily: ATP receptor P2u

  Query Match             13.4%;  Score 258.5;  DB 2;  Length 370;
  Best Local Similarity   33.2%;  Pred. No. 6.5e-15;
  Matches   69;  Conservative   35;  Mismatches   93;  Indels   11;  Gaps    4;

Qy         28 DMEKVDMNTSQEQGL--------CQFSEKYKQVYLSLAYSIIFILGLPLNGTVLWHSWGQ 79
              | :  | |:|    |        |   : :|       ||::|||||  |   |:    :
Db          8 DFQFQDSNSSLRPRLGNATANNTCIVDDSFKYNLNGAVYSVVFILGLITNSVSLFVFCFR 67

Qy         80 TKRWSCATTYLVNLMVADLLYV-LLPFLIITYSLDDRWPFGELLCKLVHFLFYINLYGSI 138
              |  |     :: || |:|||:|  ||| |  |: :  ||||: |||:    |  |:|||:
Db         68 MKMRSETAIFITNLAVSDLLFVCTLPFKIF-YNFNRHWPFGDTLCKISGTAFLTNIYGSM 126

Qy        139 LLLTCISVHQFLGVCHPLCSLPYRTRRHAWLGTSTTWALVVLQLLPTLAFSHTDYINGQM 198
              | |||||| :|| : :|  |   |||:: :  :  | ||:   :     || |:  |
Db        127 LFLTCISVDRFLAIVYPFRSRTIRTRRNSAIVCAGVWILVLSGGISASLFSTTNVNNATT 186

Qy        199 IWYDMTSQENFDR-LFAYGIVLTLSGFL 225
                ::  |:  :   |    | : : ||:
Db        187 TCFEGLSKRVWKTYLSKITIFIEVVGFI 214


RESULT 12
JC2492
G protein-coupled receptor 1 - rat
N;Alternate names: GPR-1
C;Species: Rattus norvegicus (Norway rat)
C;Date: 16-Mar-1995 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C;Accession: JC2492
R;Marchese, A.; Cheng, R.; Lee, M.C.; Porter, C.A.; Heiber, M.; Goodman, M.; George, S.R.
Biochem. Biophys. Res. Commun. 205, 1952-1958, 1994
A;Title: Mapping studies of two G protein-coupled receptor genes: An amino acid differenc
A;Reference number: JC2492; MUID:95110347; PMID:7811287
A;Accession: JC2492
A;Molecule type: mRNA
A;Residues: 1-353 <MAR>
A;Cross-references: UNIPROT:P46090; GB:S74702; NID:g786483; PIDN:AAB32978.1; PID:g786484
C;Superfamily: vertebrate rhodopsin
C;Keywords: glycoprotein; lipoprotein; phosphoprotein; receptor; thiolester bond; transme
F;74-94/Domain: transmembrane #status predicted <TM2>
F;112-133/Domain: transmembrane #status predicted <TM3>
F;134-135/Region: DR motif
F;155-175/Domain: transmembrane #status predicted <TM4>
F;209-229/Domain: transmembrane #status predicted <TM5>
F;246-266/Domain: transmembrane #status predicted <TM6>
F;295-306/Domain: transmembrane #status predicted <TM7>
F;14,273/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;150,231/Binding site: phosphate (Thr) (covalent) (by protein kinase A) #status predicte
F;330/Binding site: palmitate (Cys) (covalent) #status predicted

  Query Match             13.3%;  Score 258;  DB 2;  Length 353;
  Best Local Similarity   30.8%;  Pred. No. 6.8e-15;
  Matches   72;  Conservative   41;  Mismatches   81;  Indels   40;  Gaps    8;

Qy         26 SRDM--EKVDMNTSQEQGLCQFSEKYKQVYLS-------LAYSIIFILGLPLNGTVLW-- 74
              ||:|  |::|  :   :   |  :  : ||         | |:: |:||:| |  |:|
Db          4 SREMLFEELDNYSYALEYYSQEPDAEENVYPGIVHWISLLLYALAFVLGIPGNAIVIWFM 63

Qy         75 -HSWGQTKRWSCATTYLVNLMVADLLYVL-LPFLIITYSLDDRWPFGELLCKLVHFLFYI 132
               | :|      | : :|| :|| ::|| ||  |   :|   ||||  ||||  |:  :
Db         64 GFKWKKT----VTTLWFLNLAIADFIFVLFLPLYISYVALSFHWPFGRWLCKLNSFIAQL 119

Qy        133 NLYGSILLLTCISVHQFLGVCHPLCSLPYRTRRHAWLGTSTTWALVVLQLLPTLAFSHTD 192
              |:: |:  || ||: ::: : ||  | |:|| ::: |      | |  |   ||| |  |
Db        120 NMFSSVFFLTVISLDRYIHLIHPGLSHPHRTLKNSLLVVLFVWLLASLLGGPTLYFRDTV 179

Qy        193 YINGQMIWYDMTSQENFDRL--------------FAYGIVLTL----SGFLSLL 228
               :| ::| |:     ||                | :| :| |    | :| |:
Db        180 EVNNRIICYN-----NFQEYELTLMRHHVLTWVKFLFGYLLPLLTMSSCYLCLI 228


RESULT 13
A41795
somatostatin receptor 1 - human
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: A41795
R;Yamada, Y.; Post, S.R.; Wang, K.; Tager, H.S.; Bell, G.I.; Seino, S.
Proc. Natl. Acad. Sci. U.S.A. 89, 251-255, 1992
A;Title: Cloning and functional characterization of a family of human and mouse somatosta
A;Reference number: A41795; MUID:92108031; PMID:1346068
A;Accession: A41795
A;Molecule type: DNA
A;Residues: 1-391 <YAM>
A;Cross-references: UNIPROT:P30872; GB:M81829; NID:g307433; PIDN:AAA58247.1; PID:g307434
A;Note: sequence extracted from NCBI backbone (NCBIN:74767, NCBIP:74768)
C;Genetics:
A;Gene: GDB:SSTR1
A;Cross-references: GDB:134185; OMIM:182451
A;Map position: 14q13-14q13
A;Introns: #status absent
C;Superfamily: vertebrate rhodopsin
```

```
C;Keywords: G protein-coupled receptor; glycoprotein; hormone receptor; lipoprotein; pho
F;58-84/Domain: transmembrane #status predicted <TM1>
F;95-120/Domain: transmembrane #status predicted <TM2>
F;132-153/Domain: transmembrane #status predicted <TM3>
F;173-195/Domain: transmembrane #status predicted <TM4>
F;220-250/Domain: transmembrane #status predicted <TM5>
F;269-296/Domain: transmembrane #status predicted <TM6>
F;302-326/Domain: transmembrane #status predicted <TM7>
F;4,44,48,381/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;130-208/Disulfide bonds: #status predicted
F;172/Binding site: phosphate (Thr) (covalent) (by cAMP-dependent kinase) #status predic
F;265/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predic
F;339/Binding site: palmitate (Cys) (covalent) #status predicted

  Query Match             12.8%;  Score 248.5;  DB 2;  Length 391;
  Best Local Similarity   32.6%;  Pred. No. 5.2e-14;
  Matches   74;  Conservative   41;  Mismatches  103;  Indels    9;  Gaps    6;

Qy          7 PSRGS--RSGSRRGALLLEGASRDMEKVDMNTSQEQGLCQFSEKYKQVYLSLAYSIIFIL 64
              || ||    |  ||      ||:  ||:   | ||   | :   :    : :|  ||:: ::
Db         16 PSPGSCGEGGGSRGP--GAGAADGMEEPGRNASQNGTLSE--GQGSAILISFIYSVVCLV 71

Qy         65 GLPLNGTVLWHSWGQTKRWSCATTYLVNLMVAD-LLYVLLPFLIITYSLDDRWPFGELLC 123
              ||  |  |::      |  :    |::|| :|| || : :||| :| :|   |||| |||
Db         72 GLCGNSMVIYVILRYAKMKTATNIYILNLAIADELLMLSVPFL-VTSTLLRHWPFGALLC 130

Qy        124 KLVHFLFYINLYGSILLLTCISVHQFLGVCHPLCSLPYRTRRHAWLGTSTTWALVVLQLL 183
              :||  :  :|:: ||  || :|| ::: | ||: :  ||    | :     | | :| :|
Db        131 RLVLSVDAVNMFTSIYCLTVLSVDRYVAVVHPIKAARYRRPTVAKVVNLGVWVLSLLVIL 190

Qy        184 PTLAFSHTDYINGQMIWYDMTSQENFDR-LFAYGIVLTLSGFLSLLG 229
              | : || |   :  :  :|   |  | |  : :   | |||  :|
Db        191 PIVVFSRTAANSDGTVACNMLMPEPAQRWLVGFVLYTFLMGFLLPVG 237


RESULT 14
S15403
angiotensin II receptor type 1 - bovine
C;Species: Bos primigenius indicus x Bos primigenius taurus (cattle)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Nov-1999
C;Accession: S15403
R;Sasaki, K.; Yamano, Y.; Bardhan, S.; Iwai, N.; Murray, J.J.; Hasegawa, M.; Matsuda, Y.
Nature 351, 230-233, 1991
A;Title: Cloning and expression of a complementary DNA encoding a bovine adrenal angiote
A;Reference number: S15403; MUID:91251900; PMID:2041569
A;Accession: S15403
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-359 <SAS>
A;Cross-references: GB:X62294; NID:g43; PIDN:CAA44182.1; PID:g44
C;Superfamily: vertebrate rhodopsin

  Query Match             12.8%;  Score 247.5;  DB 2;  Length 359;
  Best Local Similarity   31.0%;  Pred. No. 5.7e-14;
  Matches   63;  Conservative   42;  Mismatches   87;  Indels   11;  Gaps    4;

Qy         34 MNTSQEQGL------CQFSEKYKQVYLSL--AYSIIFILGLPLNGTVLWHSWGQTKRWSC 85
              :|:| | |:      |  : ::  ::: :   |||||::|:  |  |:  :   |  :
Db          3 LNSSTEDGIKRIQDDCPKAGRHNYIFIMIPTLYSIIFVVGIFGNSLVVIVIYFYMKLKTV 62

Qy         86 ATTYLVNLMVADLLYVL-LPFLIITYSLDDRWPFGELLCKLVHFLFYINLYGSILLLTCI 144
              |: :|:|| :||| ::| ||   :  ::: |||||  |||:       ||| |: ||||:
Db         63 ASVFLLNLALADLCFLLTLPLWAVYTAMEYRWPFGNYLCKIASASVSFNLYASVFLLTCL 122

Qy        145 SVHQFLGVCHPLCSLPYRTRRHAWLGTSTTWALVVLQLLPTLAFSHTDYINGQMIWYDMT 204
              |: ::| : ||: |   ||   | :     | |  |  |||:   :  :|    |
Db        123 SIDRYLAIVHPMKSRLRRTMLVAKVTCIIIWLLAGLASLPTIIHRNVFFIENTNITVCAF 182

Qy        205 SQENFDRLFAYGIVLT--LSGFL 225
                |: :     |: ||  : |||
Db        183 HYESQNSTLPVGLGLTKNILGFL 205


RESULT 15
I48705
proteinase activated receptor 2 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I48705
R;Nystedt, S.; Larsson, A.K.; Aberg, H.; Sundelin, J.
J. Biol. Chem. 270, 5950-5955, 1995
A;Title: The mouse proteinase-activated receptor-2 cDNA and gene. Molecular cloning and f
A;Reference number: I48705; MUID:95197620; PMID:7890726
A;Accession: I48705
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-399 <RES>
A;Cross-references: UNIPROT:P55086; EMBL:Z48043; NID:g663020; PIDN:CAA88097.1; PID:g66302
C;Superfamily: ATP receptor P2u

  Query Match             12.7%;  Score 246;  DB 2;  Length 399;
  Best Local Similarity   35.1%;  Pred. No. 8.8e-14;
  Matches   68;  Conservative   34;  Mismatches   80;  Indels   12;  Gaps    7;

Qy         48 KYKQVYLSLAYSIIFILGLPLNGTVLWHSWGQTKRWSCATTYLVNLMVADLLYVLLPFLI 107
              |   |:| : | |:|::||| ||  ||    :||:   |  |: || :|||| |:  |
Db         74 KLTTVFLPVVYIIVFVIGLPSNGMALWIFLFRTKKKHPAVIYMANLALADLLSVIWFPLK 133

Qy        108 ITYSL-DDRWPFGELLCKLVHFLFYINLYGSILLLTCISVHQFLGVCHPLCSLPYRTRRH 166
              |:| |  : | :|| |||::   || |:| ||| :||:|| ::  : :|:   | | : :
Db        134 ISYHLHGNNWVYGEALCKVLIGFFYGNMYCSILFMTCLSVQRYWVIVNPM-GHP-RKKAN 191

Qy        167 AWLGTS-TTWALVVLQLLPTLAFSHTDYINGQMI--WYDMTSQENF-DRLFAYGIVLTLS 222
              :| |   | |: |  :|       | ||     |  :|:  :|     :| | : | :
Db        192 IAVGVSLAIWLLIFLVTIPLYVMKQTIYIPALNITTCHDVLPEEVLVGDMFNYFLSLAIG 251

Qy        223 GFLSLLGHFGVLFT 236
               ||     | | |
Db        252 VFL-----FPALLT 260


Search completed: November  4, 2004, 16:57:58
Job time : 42 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 4, 2004, 16:51:19 ; Search time 191 Seconds
(without alignments)
1084.476 Million cell updates/sec

Title: US-10-763-972-2
Perfect score: 1936
Sequence: 1 MLSILLPSRGSRSGSRRGAL.....QNKLGEHPAGRKRCPGLNRS 360

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1936	100.0	361	2	Q711G2	Q711g2 homo sapien
2	1936	100.0	361	2	CAC87811	Cac87811 homo sapi
3	447	23.1	328	1	P2Y3_CHICK	Q98907 gallus gall
4	447	23.1	328	1	P2Y3_MELGA	O93361 meleagris g
5	421	21.7	374	2	O57466	O57466 meleagris g
6	416	21.5	537	1	P2Y8_XENLA	P79928 xenopus lae
7	414	21.4	537	2	Q7ZWQ7	Q7zwq7 xenopus lae
8	400	20.7	328	1	P2Y6_RAT	Q63371 rattus norv
9	400	20.7	328	2	AAH72520	Aah72520 rattus no
10	395	20.4	328	1	P2Y6_MOUSE	Q9erk9 mus musculu
11	395	20.4	328	2	AAH64095	Aah64095 mus muscu
12	388	20.0	361	1	P2Y4_RAT	O35811 rattus norv
13	387.5	20.0	328	1	P2Y6_HUMAN	Q15077 homo sapien
14	387.5	20.0	328	2	AAP35417	Aap35417 homo sapi
15	387.5	20.0	377	1	P2Y2_HUMAN	P41231 homo sapien
16	386	19.9	361	1	P2Y4_MOUSE	Q9jjs7 mus musculu
17	386	19.9	361	2	BAC36314	Bac36314 mus muscu
18	381.5	19.7	347	2	Q7ZZA4	Q7zza4 brachydanio
19	371	19.2	373	1	P2Y2_MOUSE	P35383 mus musculu
20	367	19.0	365	1	P2Y4_HUMAN	P51582 homo sapien
21	366.5	18.9	374	1	P2Y2_RAT	P41232 rattus norv
22	366.5	18.9	374	2	AAH61754	Aah61754 rattus no
23	363.5	18.8	349	2	Q6P852	Q6p852 xenopus tro
24	363.5	18.8	349	2	AAH61378	Aah61378 xenopus t
25	359	18.5	357	2	Q9DE05	Q9de05 raja erinac
26	346	17.9	362	1	P2YR_CHICK	P34996 gallus gall
27	346	17.9	362	1	P2YR_MELGA	P49652 meleagris g
28	329.5	17.0	361	2	Q90X57	Q90x57 xenopus lae
29	329.5	17.0	373	1	P2YR_CAVPO	P59902 cavia porce
30	329.5	17.0	373	1	P2YR_RAT	P49651 rattus norv
31	328	16.9	373	1	P2YR_HUMAN	P47900 homo sapien
32	326.5	16.9	373	1	P2YR_BOVIN	P48042 bos taurus
33	320	16.5	373	1	P2YR_MOUSE	P49650 mus musculu
34	320	16.5	373	2	Q8BMJ5	Q8bmj5 mus musculu
35	320	16.5	373	2	BAC28413	Bac28413 mus muscu
36	320	16.5	373	2	BAC29506	Bac29506 mus muscu
37	291.5	15.1	337	2	Q6Y1R5	Q6y1r5 rattus norv
38	291.5	15.1	337	2	AAP32736	Aap32736 rattus no
39	288	14.9	337	2	Q6IYF8	Q6iyf8 mus musculu
40	288	14.9	337	2	AAT10591	Aat10591 mus muscu
41	282.5	14.6	308	1	P2Y5_CHICK	P32250 gallus gall
42	280	14.5	344	1	P2Y5_MOUSE	Q8bmc0 mus musculu
43	280	14.5	344	2	AAH69991	Aah69991 mus muscu
44	279.5	14.4	121	2	Q8HYZ8	Q8hyz8 bos taurus
45	278.5	14.4	337	1	GP80_HUMAN	Q96p68 homo sapien

ALIGNMENTS

```
RESULT 1
Q711G2
ID   Q711G2      PRELIMINARY;      PRT;   361 AA.
AC   Q711G2;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Nucleoside/nucleotide receptor.
GN   Name=P2Y2-like;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Blood;
RA   Bruss M., Bonisch H., Kugelgen I.;
RL   Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Blood;
RA   Bruess M.;
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ345013; CAC87811.1; -.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR002286; P2_purnocptor.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PRINTS; PR01157; P2YPURNOCPTR.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   361 AA;  40633 MW;  3992A1A1EF512AFE CRC64;

  Query Match          100.0%;  Score 1936;  DB 2;  Length 361;
  Best Local Similarity  100.0%;  Pred. No. 1.7e-134;
  Matches  360;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLSILLPSRGSRSGSRRGALLLEGASRDMEKVDMNTSQEQGLCQFSEKYKQVYLSLAYSI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLSILLPSRGSRSGSRRGALLLEGASRDMEKVDMNTSQEQGLCQFSEKYKQVYLSLAYSI 60

Qy         61 IFILGLPLNGTVLWHSWGQTKRWSCATTYLVNLMVADLLYVLLPFLIITYSLDDRWPFGE 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 IFILGLPLNGTVLWHSWGQTKRWSCATTYLVNLMVADLLYVLLPFLIITYSLDDRWPFGE 120

Qy        121 LLCKLVHFLFYINLYGSILLLTCISVHQFLGVCHPLCSLPYRTRRHAWLGTSTTWALVVL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLCKLVHFLFYINLYGSILLLTCISVHQFLGVCHPLCSLPYRTRRHAWLGTSTTWALVVL 180

Qy        181 QLLPTLAFSHTDYINGQMIWYDMTSQENFDRLFAYGIVLTLSGFLSLLGHFGVLFTDGQE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 QLLPTLAFSHTDYINGQMIWYDMTSQENFDRLFAYGIVLTLSGFLSLLGHFGVLFTDGQE 240
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Qy        241 PDQARGEPHEDRQHSPSQVHPDHPTGVWPLHPLFCALPYHSLLLPHHLLSAFSGLPALDG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 PDQARGEPHEDRQHSPSQVHPDHPTGVWPLHPLFCALPYHSLLLPHHLLSAFSGLPALDG 300

Qy        301 SQCGLQDMEASGECEQLPQPSPVLSFKGGKNRVRLLQKLRQNKLGEHPAGRKRCPGLNRS 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 SQCGLQDMEASGECEQLPQPSPVLSFKGGKNRVRLLQKLRQNKLGEHPAGRKRCPGLNRS 360


RESULT 2
CAC87811
ID   CAC87811    PRELIMINARY;      PRT;   361 AA.
AC   CAC87811;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   Nucleoside/nucleotide receptor.
GN   P2Y2-LIKE.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Blood;
RA   Bruss M., Bonisch H., Kugelgen I.;
RT   "Molecular identification and functional characterization of a new G
RT   protein-coupled nucleoside-/nucleotide receptor.";
RL   Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Blood;
RA   Bruess M.;
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ345013; CAC87811.1; -.
KW   Receptor.
SQ   SEQUENCE   361 AA;  40633 MW;  3992A1A1EF512AFE CRC64;

  Query Match           100.0%;  Score 1936;  DB 2;  Length 361;
  Best Local Similarity  100.0%;  Pred. No. 1.7e-134;
  Matches  360;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLSILLPSRGSRSGSRRGALLLEGASRDMEKVDMNTSQEQGLCQFSEKYKQVYLSLAYSI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLSILLPSRGSRSGSRRGALLLEGASRDMEKVDMNTSQEQGLCQFSEKYKQVYLSLAYSI 60

Qy         61 IFILGLPLNGTVLWHSWGQTKRWSCATTYLVNLMVADLLYVLLPFLIITYSLDDRWPFGE 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 IFILGLPLNGTVLWHSWGQTKRWSCATTYLVNLMVADLLYVLLPFLIITYSLDDRWPFGE 120

Qy        121 LLCKLVHFLFYINLYGSILLLTCISVHQFLGVCHPLCSLPYRTRRHAWLGTSTTWALVVL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLCKLVHFLFYINLYGSILLLTCISVHQFLGVCHPLCSLPYRTRRHAWLGTSTTWALVVL 180

Qy        181 QLLPTLAFSHTDYINGQMIWYDMTSQENFDRLFAYGIVLTLSGFLSLLGHFGVLFTDGQE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 QLLPTLAFSHTDYINGQMIWYDMTSQENFDRLFAYGIVLTLSGFLSLLGHFGVLFTDGQE 240

Qy        241 PDQARGEPHEDRQHSPSQVHPDHPTGVWPLHPLFCALPYHSLLLPHHLLSAFSGLPALDG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 PDQARGEPHEDRQHSPSQVHPDHPTGVWPLHPLFCALPYHSLLLPHHLLSAFSGLPALDG 300

Qy        301 SQCGLQDMEASGECEQLPQPSPVLSFKGGKNRVRLLQKLRQNKLGEHPAGRKRCPGLNRS 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 SQCGLQDMEASGECEQLPQPSPVLSFKGGKNRVRLLQKLRQNKLGEHPAGRKRCPGLNRS 360


RESULT 3
P2Y3_CHICK
ID   P2Y3_CHICK     STANDARD;      PRT;   328 AA.
AC   Q98907;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   P2Y purinoceptor 3 (P2Y3) (Nucleoside diphosphate receptor).
GN   Name=P2RY3;
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=96319774; PubMed=8700132;
RA   Webb T.E., Henderson D., King B.F., Wang S., Simon J., Bateson A.N.,
RA   Burnstock G., Barnard E.A.;
RT   "A novel G protein-coupled P2 purinoceptor (P2Y3) activated
RT   preferentially by nucleoside diphosphates.";
RL   Mol. Pharmacol. 50:258-265(1996).
CC   -!- FUNCTION: Receptor for extracellular ADP > UTP > ATP = UDP. The
CC       activity of this receptor is mediated by G proteins which activate
CC       a phosphatidylinositol-calcium second messenger system.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X98283; CAA66930.1; -.
DR   HSSP; P34996; 1DDD.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR000371; P2Y3_purnocptor.
DR   InterPro; IPR002286; P2_purnocptor.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Glycoprotein; Transmembrane.
FT   DOMAIN       1     22       Extracellular (Potential).
FT   TRANSMEM     23    43       1 (Potential).
FT   DOMAIN       44    57       Cytoplasmic (Potential).
FT   TRANSMEM     58    78       2 (Potential).
FT   DOMAIN       79    96       Extracellular (Potential).
FT   TRANSMEM     97    117      3 (Potential).
FT   DOMAIN       118   139      Cytoplasmic (Potential).
FT   TRANSMEM     140   160      4 (Potential).
FT   DOMAIN       161   189      Extracellular (Potential).
FT   TRANSMEM     190   210      5 (Potential).
FT   DOMAIN       211   231      Cytoplasmic (Potential).
FT   TRANSMEM     232   252      6 (Potential).
FT   DOMAIN       253   275      Extracellular (Potential).
FT   TRANSMEM     276   298      7 (Potential).
FT   DOMAIN       299   323      Extracellular (Potential).
FT   CARBOHYD     5     5        N-linked (GlcNAc. . .) (Potential).
FT   DISULFID     94    172      By similarity.
SQ   SEQUENCE   328 AA;  37586 MW;  7A3BF1C91F54FAAB CRC64;

  Query Match           23.1%;  Score 447;  DB 1;  Length 328;
  Best Local Similarity  45.9%;  Pred. No. 6.4e-25;
  Matches   85;  Conservative   31;  Mismatches   67;  Indels    2;  Gaps    2;

Qy         43 CQFSEKYKQVYLSLAYSIIFILGLPLNGTVLWHSWGQTKRWSCATTYLVNLMVADLLYVL 102
              | | |::||| | | ||::|:|||||  |:   |   |  :  | |::|| :||||||
Db         13 CTFHEEFKQVLLPLVYSVVFLLGLPLNAVVIGQIWLARKALTRTTIYMLNLAMADLLYVC 72

Qy        103 -LPFLIITYSLDDRWPFGELLCKLVHFLFYINLYGSILLLTCISVHQFLGVCHPLCSL-P 160
               ||- ||  |:  | ||||:  || | | || ||:|||| |||||| :::|:|||| |
Db         73 SLPLLIYNYTQKDYWPFGDFTCKFVRFQFYTNLHGSILFLTCISVQRYMGICHPLASWHK 132

Qy        161 YRTRRHAWLGTSTTWALVVLQLLPTLAFSHTDYINGQMIWYDMTSQENFDRLFAYGIVLT 220
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Db        133 KKGKKLTWLVCAAVWFIVIAQCLPTFVFASTGTQRNRTVCYDLSPPDRSTSYFPYGITLT 192

Qy        221 LSGFL 225
Db        193 ITGFL 197
```

RESULT 4
P2Y3_MELGA
ID   P2Y3_MELGA   STANDARD;   PRT;   328 AA.
AC   O93361;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   P2Y purinoceptor 3 (P2Y3) (Nucleoside diphosphate receptor).
GN   Name=P2RY3;
OS   Meleagris gallopavo (Common turkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Meleagris.
OX   NCBI_TaxID=9103;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98401046; PubMed=9730913;
RA   Li Q., Olesky M., Palmer R.K., Harden T.K., Nicholas R.A.;
RT   "Evidence that the p2y3 receptor is the avian homologue of the
RT   mammalian P2Y6 receptor.";
RL   Mol. Pharmacol. 54:541-546(1998).
CC   -!- FUNCTION: Receptor for extracellular UDP > ADP = UTP. The activity
CC   of this receptor is mediated by G proteins which activate a
CC   phosphatidylinositol-calcium second messenger system.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC   ---
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---
DR   EMBL; AF069555; AAC23863.1; -.
DR   HSSP; P34996; 1DDD.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR000371; P2Y3_purnocptor.
DR   InterPro; IPR002286; P2_purnocptor.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Glycoprotein; Transmembrane.

FT	DOMAIN	1	22	Extracellular (Potential).
FT	TRANSMEM	23	43	1 (Potential).
FT	DOMAIN	44	57	Cytoplasmic (Potential).
FT	TRANSMEM	58	78	2 (Potential).
FT	DOMAIN	79	96	Extracellular (Potential).
FT	TRANSMEM	97	117	3 (Potential).
FT	DOMAIN	118	139	Cytoplasmic (Potential).
FT	TRANSMEM	140	160	4 (Potential).
FT	DOMAIN	161	189	Extracellular (Potential).
FT	TRANSMEM	190	210	5 (Potential).
FT	DOMAIN	211	231	Cytoplasmic (Potential).
FT	TRANSMEM	232	252	6 (Potential).
FT	DOMAIN	253	275	Extracellular (Potential).
FT	TRANSMEM	276	298	7 (Potential).
FT	DOMAIN	299	323	Extracellular (Potential).
FT	CARBOHYD	5	5	N-linked (GlcNAc. . .) (Potential).
FT	DISULFID	94	172	By similarity.

SQ   SEQUENCE   328 AA; 37594 MW; B74D49B99C7164A5 CRC64;

Query Match 23.1%; Score 447; DB 1; Length 328;
Best Local Similarity 44.6%; Pred. No. 6.4e-25;
Matches 86; Conservative 32; Mismatches 73; Indels 2; Gaps 2;

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Qy         35 NTSQEQGLCQFSEKYKQVYLSLAYSIIFILGLPLNGTVLWHSWGQTKRWSCATTYLVNLM 94
Db          5 NFTAGRNSCTFQEEFKQVLLPLVYSVVFLLGLPLNAVVIGQIWLARKALTRTTIYMLNLA 64

Qy         95 VADLLYVL-LPFLIITYSLDDRWPFGELLCKLVHFLFYINLYGSILLLTCISVHQFLGVC 153
Db         65 TADLLYVCSLPLLIYNYTQKDYWPFGDFTCKFVRFQFYTNLHGSILFLTCISVQRYMGIC 124

Qy        154 HPLCSL-PYRTRRHAWLGTSTTWALVVLQLLPTLAFSHTDYINGQMIWYDMTSQENFDRL 212
Db        125 HPLASWHKKKGKKLTWLVCAAVWFIVIAQCLPTFVFASTGTQRNRTVCYDLSPPDRSASY 184

Qy        213 FAYGIVLTLSGFL 225
Db        185 FPYGITLTITGFL 197
```

RESULT 5
O57466
ID   O57466   PRELIMINARY;   PRT;   374 AA.
AC   O57466;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   G protein coupled P2Y nucleotide receptor.
GN   Name=tp2y;
OS   Meleagris gallopavo (Common turkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Meleagris.
OX   NCBI_TaxID=9103;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Blood;
RX   MEDLINE=98086419; PubMed=9415702;
RA   Boyer J.L., Waldo G.L., Harden T.K.;
RT   "Molecular cloning and expression of an avian G protein-coupled P2Y
RT   receptor.";
RL   Mol. Pharmacol. 52:928-934(1997).
DR   EMBL; AF031897; AAC60339.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0045028; F:purinergic nucleotide receptor activity, G-. . .; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR000018; P2Y4_purnocptor.
DR   InterPro; IPR002286; P2_purnocptor.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PRINTS; PR01066; P2Y4PRNOCPTR.
DR   PRINTS; PR01157; P2YPURNOCPTR.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   374 AA; 42594 MW; 849C465722BDD02B CRC64;

Query Match 21.7%; Score 421; DB 2; Length 374;
Best Local Similarity 40.3%; Pred. No. 6e-23;
Matches 81; Conservative 40; Mismatches 72; Indels 8; Gaps 3;

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Qy         36 TSQEQGLCQFSEKYKQVYLSLAYSIIFILGLPLNGTVLWHSWGQTKRWSCATTYLVNLMV 95
Db         26 TAAAEAKCVFNEEFKFILLPISYGIVFVVGLPLNSWAMWIFVSRMRPWNATTTYMFNLAI 85

Qy         96 ADLLYVL-LPFLIITYSLDDRWPFGELLCKLVHFLFYINLYGSILLLTCISVHQFLGVCH 154
Db         86 SDTLYVFSLPTLVYYYADRNNWPFGKVFCKIVRFLFYANLYSSILFLTCISVHRYMGICH 145

Qy        155 PLCSLPYRTRRHAWLGTSTTWALVVLQLLPTLAFSHTDYINGQMIWYDMTSQENFDRLFA 214
Db        146 PIRSLKWVKTKHARLICVGVWLVVTICLIPNLIFVTTSSKDNSTLCHDTTKPEEFDHYVH 205
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Qy        215 YGIVLTLSGFLSLLGHFGVLF 235
              |      |  ::||  ||: |
Db        206 YS-----SSIMALL--FGIPF 219


RESULT 6
P2Y8_XENLA
ID   P2Y8_XENLA     STANDARD;      PRT;   537 AA.
AC   P79928;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   P2Y purinoceptor 8 (P2Y8).
GN   Name=P2RY8;
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Neural plate;
RX   MEDLINE=97284734; PubMed=9139711;
RA   Bogdanov Y.D., Dale L., King B.F., Whittock N., Burnstock G.;
RT   "Early expression of a novel nucleotide receptor in the neural plate
RT   of Xenopus embryos.";
RL   J. Biol. Chem. 272:12583-12590(1997).
CC   -!- FUNCTION: Receptor for extracellular ATP, UTP, CTP, GTP and ITP.
CC       The activity of this receptor is mediated by G proteins which
CC       activate a phosphatidylinositol-calcium second messenger system.
CC       May play a key role in the early development of neural tissue.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X99953; CAA68213.1; -.
DR   HSSP; P34996; 1DDD.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR000018; P2Y4_purnocptor.
DR   InterPro; IPR002286; P2_purnocptor.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Glycoprotein; Transmembrane.
FT   DOMAIN        1     49       Extracellular (Potential).
FT   TRANSMEM     50     70       1 (Potential).
FT   DOMAIN       71     79       Cytoplasmic (Potential).
FT   TRANSMEM     80    100       2 (Potential).
FT   DOMAIN      101    118       Extracellular (Potential).
FT   TRANSMEM    119    139       3 (Potential).
FT   DOMAIN      140    161       Cytoplasmic (Potential).
FT   TRANSMEM    162    182       4 (Potential).
FT   DOMAIN      183    210       Extracellular (Potential).
FT   TRANSMEM    211    231       5 (Potential).
FT   DOMAIN      232    254       Cytoplasmic (Potential).
FT   TRANSMEM    255    275       6 (Potential).
FT   DOMAIN      276    292       Extracellular (Potential).
FT   TRANSMEM    293    316       7 (Potential).
FT   DOMAIN      317    537       Cytoplasmic (Potential).
FT   DISULFID    116    193       By similarity.
FT   CARBOHYD     26     26       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     29     29       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   537 AA;  62024 MW;  B2CF24812F3C19F2 CRC64;
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  Query Match           21.5%;  Score 416;  DB 1;  Length 537;
  Best Local Similarity  31.8%;  Pred. No. 2e-22;
  Matches  110;  Conservative   59;  Mismatches  139;  Indels   38;  Gaps   10;

Qy         31 KVDMN-TSQEQGLCQFSEKYKQVYLSLAYSIIFILGLPLNGTVLWHSWGQTKRWSCATTY 89
              |: || |:  : :| | | :| : | ::|| :|::|||||   :|    : : |:  | |
Db         22 KLLMNLTNDTEDICVFDEGFKFLLLPVSYSAVFMVGLPLNIAAMWIFIAKMRPWNPTTVY 81

Qy         90 LVNLMVADLLYVL-LPFLIITYSLDDRWPFGELLCKLVHFLFYINLYGSILLLTCISVHQ 148
              : || ::| |||| || |:  |:  : ||||:|||| |||| ||| ||| |||||||:
Db         82 MFNLALSDTLYVLSLPTLVYYYADKNNWPFGEVLCKLVRFLFYANLYSSILFLTCISVHR 141

Qy        149 FLGVCHPLCSLPYRTRRHAWLGTSTTWALVVLQLLPTLAFSHTDYINGQMIWYDMTSQEN 208
              : |||||: ||     :||::  :  |  | | |:| | |           | :| |  |:
Db        142 YRGVCHPITSLRRMNAKHAYVICALVWLSVTLCLVPNLIFVTVSPKVKNTICHDTTRPED 201

Qy        209 FDRLFAY--GIVLTLSGF--LSLLGHFGVLFTDGQEPDQARGEPHEDRQHSPSQVHPDHP 264
              | |   |  |:  | |   | : | :|:: :  :|  :      ::|  ||
Db        202 FARYVEYSTAIMCLLFGIPCLIIAGCYGLMTRELMKPIVS-----GNQQTLPSYKKRSIK 256

Qy        265 TGVWPLHPLFCALPYHSLLLPHHLLSAFSGLPALDGSQC----------GLQDMEASGE 313
              |       :|  : :    :| |:          | | :|             : : ::
Db        257 T------IIFVMIAFAICFMPFHITRTLYYYARLLGIKCYALNVINVTYKVTRPLASANS 310

Qy        314 CEQLPQPSPVLSF-KGGKNRVRLLQKLRQNKLGEHPAGRKRCPGLN 358
              |       |:| |    : | ||:: :|:          :||   |
Db        311 C-----IDPILYFLANDRYRRRLIRTVRRRS----SVPNRRCMHTN 347


RESULT 7
Q7ZWQ7
ID   Q7ZWQ7      PRELIMINARY;      PRT;   537 AA.
AC   Q7ZWQ7;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   P2ry4-prov protein.
GN   Name=p2ry4-prov;
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RX   MEDLINE=22341132; PubMed=12454917;
RA   Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA   Richardson P.;
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RT   "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT   initiative.";
RL   Dev. Dyn. 225:384-391(2002).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RA   Klein S., Strausberg R.;
RL   Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC046837; AAH46837.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0045028; F:purinergic nucleotide receptor activity, G-. . .; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR000018; P2Y4_purnocptor.
DR   InterPro; IPR002286; P2_purnocptor.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PRINTS; PR01066; P2Y4PRNOCPTR.
DR   PRINTS; PR01157; P2YPURNOCPTR.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
SQ   SEQUENCE   537 AA;  61981 MW;  B030F67D76CB9622 CRC64;

  Query Match             21.4%;  Score 414;  DB 2;  Length 537;
  Best Local Similarity   31.8%;  Pred. No. 2.8e-22;
  Matches  109;  Conservative   58;  Mismatches  138;  Indels   38;  Gaps   10;

Qy         34 MN-TSQEQGLCQFSEKYKQVYLSLAYSIIFILGLPLNGTVLWHSWGQTKRWSCATTYLVN 92
              ||:|:  : :| | | :| : | ::|| :|::|||||   :|    : : |:  | |: |
Db         25 MNLTNDTEDICVFDEGFKFLLLPVSYSAVFMVGLPLNIAAMWIFIAKMRPWNPTTVYMFN 84

Qy         93 LMVADLLYVL-LPFLIITYSLDDRWPFGELLCKLVHFLFYINLYGSILLLTCISVHQFLG 151
              | ::| |||| || |:  |:  : |||||:||||| |||| ||| ||| |||||||:: |
Db         85 LALSDTLYVLSLPTLVYYYADKNNWPFGEVLCKLVRFLFYANLYSSILFLTCISVHRYRG 144

Qy        152 VCHPLCSLPYRTRRHAWLGTSTTWALVVLQLLPTLAFSHTDYINGQMIWYDMTSQENFDR 211
              ||||: ||      :||::  :  |  | | |:| | |           | :| |  |:| |
Db        145 VCHPITSLRRMNAKHAYVICALVWLSVTLCLVPNLIFVTVSPKVKNTICHDTTRPEDFAR 204

Qy        212 LFAY--GIVLTLSGF--LSLLGHFGVLFTDGQEPDQARGEPHEDRQHSPSQVHPDHPTGV 267
                 |   |:  | |   | : | :|::  :  :|  :      ::|  ||       |
Db        205 YVEYSTAIMCLLFGIPCLIIAGCYGLMTRELMKPIVS-----GNQQTLPSYKKRSIKT-- 257

Qy        268 WPLHPLFCALPYHSLLLPHHLLSAFSGLPALDGSQC----------GLQDMEASGECEQ 316
                :|  : :    :| |:          | | :|          : : ::  |
Db        258 ----IIFVMIAFAICFMPFHITRTLYYYARLLGIKCYALNVINVTYKVTRPLASANSC-- 311

Qy        317 LPQPSPVLSF-KGGKNRVRLLQKLRQNKLGEHPAGRKRCPGLN 358
                  |:| |    : | ||:: :|:          :||   |
Db        312 ---IDPILYFLANDRYRRRLIRTVRRRS----SVPNRRCMHTN 347


RESULT 8
P2Y6_RAT
ID   P2Y6_RAT       STANDARD;      PRT;   328 AA.
AC   Q63371;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   P2Y purinoceptor 6 (P2Y6).
GN   Name=P2ry6;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Aortic smooth muscle;
RX   MEDLINE=96064682; PubMed=7592819;
RA   Chang K., Hanaoka K., Kumada M., Takuwa Y.;
RT   "Molecular cloning and functional analysis of a novel P2 nucleotide
RT   receptor.";
RL   J. Biol. Chem. 270:26152-26158(1995).
CC   -!- FUNCTION: Receptor for extracellular UTP > ADP = 2-methylthio-ATP
CC       > ADP-beta-S > ATP = ATP-gamma-S. The activity of this receptor is
CC       mediated by G proteins which activate a phosphatidylinositol-
CC       calcium second messenger system. Functionally coupled to
CC       phospholipase C.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: Abundantly expressed in various tissues
CC       including lung, stomach, intestine, spleen, mesentery, heart, and,
CC       most prominently, aorta.
CC   -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; D63665; BAA09816.1; -.
DR   PIR; I55450; I55450.
DR   HSSP; P34996; 1DDD.
DR   RGD; 620269; P2ry6.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR001973; P2Y6_purnocptor.
DR   InterPro; IPR002286; P2_purnocptor.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Glycoprotein; Transmembrane.
FT   DOMAIN        1     27       Extracellular (Potential).
FT   TRANSMEM     28     48       1 (Potential).
FT   DOMAIN       49     62       Cytoplasmic (Potential).
FT   TRANSMEM     63     83       2 (Potential).
FT   DOMAIN       84    101       Extracellular (Potential).
FT   TRANSMEM    102    122       3 (Potential).
FT   DOMAIN      123    144       Cytoplasmic (Potential).
FT   TRANSMEM    145    165       4 (Potential).
FT   DOMAIN      166    194       Extracellular (Potential).
FT   TRANSMEM    195    215       5 (Potential).
FT   DOMAIN      216    236       Cytoplasmic (Potential).
FT   TRANSMEM    237    257       6 (Potential).
FT   DOMAIN      258    280       Extracellular (Potential).
FT   TRANSMEM    281    303       7 (Potential).
FT   DOMAIN      304    328       Extracellular (Potential).
FT   DISULFID     99    177       By similarity.
FT   CARBOHYD      5      5       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    173    173       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   328 AA;  36677 MW;  58EBE1997038BA5B CRC64;

  Query Match             20.7%;  Score 400;  DB 1;  Length 328;
  Best Local Similarity   32.5%;  Pred. No. 1.8e-21;
  Matches  108;  Conservative   53;  Mismatches  137;  Indels   34;  Gaps    9;

Qy         29 MEKVDMNTSQEQGL----CQFSEKYKQVYLSLAYSIIFILGLPLNGTVLWHSWGQTKRWS 84
              ||: |  | |  ||    | : | :|:: |   ||:: ::|||||  |:       :  :
Db          1 MER-DNGTIQAPGLPPTTCVYREDFKRLLLPPVYSVVLVVGLPLNVCVIAQICASRRTLT 59

Qy         85 CATTYLVNLMVADLLYVL-LPFLIITYSLDDRWPFGELLCKLVHFLFYINLYGSILLLTC 143
               :  | :|| :|||||   || ||  |:  | ||||:| |:|| |||| ||:|||| |||
Db         60 RSAVYTLNLALADLLYACSLPLLIYNYARGDHWPFGDLACRLVRFLFYANLHGSILFLTC 119

Qy        144 ISVHQFLGVCHPLCSLPYR-TRRHAWLGTSTTWALVVLQLLPTLAFSHTDYINGQMIWYD 202
              ||  ::||:||||      |  || ||:     | :|  | |||  |: |     : : ||
Db        120 ISFQRYLGICHPLAPWHKRGGRRAAWVVCGVVWLVVTAQCLPTAVFAATGIQRNRTVCYD 179

Qy        203 MTSQENFDRLFAYGIVLTLSGFL----SLLGHFGVLFTDGQEPDQARGEPHEDRQHSPSQ 258
              ::       |   ||: ||: |||    :|| :  :        |   |   ::|:   ::
Db        180 LSPPILSTRYLPYGMALTVIGFLLPFTALLACYCRMARRLCRQDGPAGPVAQERRSKAAR 239

Qy        259 VHPDHPTGVWPLHPLFCALPYHSLLLPHHLL-SAFSGLPALDGSQCGLQDMEASGECEQL 317
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Db        240 M------------AVVVAAVFVISFLPFHITKTAYLAVRSTPGVSCPVLETFAAAYKGTR 287

Qy        318 PQPS------PVLSF----KGGKNRVRLLQKL 339
Db        288 PFASANSVLDPILFYFTQQKFRRQPHDLLQKL 319
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RESULT 9
AAH72520
ID AAH72520 PRELIMINARY; PRT; 328 AA.
AC AAH72520;
DT 01-JUN-2004 (TrEMBLrel. 27, Created)
DT 01-JUN-2004 (TrEMBLrel. 27, Last sequence update)
DT 01-JUN-2004 (TrEMBLrel. 27, Last annotation update)
DE P2ry6 protein.
GN P2RY6.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC072520; AAH72520.1; -.
SQ SEQUENCE 328 AA; 36677 MW; 58EBE1997038BA5B CRC64;

Query Match 20.7%; Score 400; DB 2; Length 328;
Best Local Similarity 32.5%; Pred. No. 1.8e-21;
Matches 108; Conservative 53; Mismatches 137; Indels 34; Gaps 9;

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Qy         29 MEKVDMNTSQEQGL----CQFSEKYKQVYLSLAYSIIFILGLPLNGTVLWHSWGQTKRWS 84
Db          1 MER-DNGTIQAPGLPPTTCVYREDFKRLLLPPVYSVVLVVGLPLNVCVIAQICASRRTLT 59

Qy         85 CATTYLVNLMVADLLYVL-LPFLIITYSLDDRWPFGELLCKLVHFLFYINLYGSILLLTC 143
Db         60 RSAVYTLNLALADLLYACSLPLLIYNYARGDHWPFGDLACRLVRFLFYANLHGSILFLTC 119

Qy        144 ISVHQFLGVCHPLCSLPYR-TRRHAWLGTSTTWALVVLQLLPTLAFSHTDYINGQMIWYD 202
Db        120 ISFQRYLGICHPLAPWHKRGGRRAAWVVCGVVWLVVTAQCLPTAVFAATGIQRNRTVCYD 179

Qy        203 MTSQENFDRLFAYGIVLTLSGFL----SLLGHFGVLFTDGQEPDQARGEPHEDRQHSPSQ 258
Db        180 LSPPILSTRYLPYGMALTVIGFLLPFTALLACYCRMARRLCRQDGPAGPVAQERRSKAAR 239
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Qy        259 VHPDHPTGVWPLHPLFCALPYHSLLLPHHLL-SAFSGLPALDGSQCGLQDMEASGECEQL 317
Db        240 M------------AVVVAAVFVISFLPFHITKTAYLAVRSTPGVSCPVLETFAAAYKGTR 287

Qy        318 PQPS------PVLSF----KGGKNRVRLLQKL 339
Db        288 PFASANSVLDPILFYFTQQKFRRQPHDLLQKL 319
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RESULT 10
P2Y6_MOUSE
ID P2Y6_MOUSE STANDARD; PRT; 328 AA.
AC Q9ERK9;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE P2Y purinoceptor 6 (P2Y6).
GN Name=P2ry6;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvEv;
RX MEDLINE=21160052; PubMed=11259526;
RA Lazarowski E.R., Rochelle L.G., O'Neal W.K., Ribeiro C.M.P.,
RA Grubb B.R., Zhang V., Harden T.K., Boucher R.C.;
RT "Cloning and functional characterization of two murine uridine
RT nuclectide receptors reveal a potential target for correcting ion
RT transport deficiency in cystic fibrosis gallbladder.";
RL J. Pharmacol. Exp. Ther. 297:43-49(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Receptor for extracellular UTP > ADP = 2-methylthio-ATP
CC > ADP-beta-S > ATP = ATP-gamma-S. The activity of this receptor is
CC mediated by G proteins which activate a phosphatidylinositol-
CC calcium second messenger system. Functionally coupled to
CC phospholipase C (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC ----------
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC ----------
DR EMBL; AF298899; AAG24619.1; -.
DR EMBL; BC027331; AAH27331.1; -.

```
DR   MGD; MGI:2673874; P2ry6.
DR   GO; GO:0019103; F:pyrimidine nucleotide binding; IC.
DR   GO; GO:0045029; F:UDP-activated nucleotide receptor activity; IDA.
DR   GO; GO:0030321; P:transepithelial chloride transport; IDA.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR001973; P2Y6_purnocptor.
DR   InterPro; IPR002286; P2_purnocptor.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Glycoprotein; Transmembrane.
FT   DOMAIN        1     27       Extracellular (Potential).
FT   TRANSMEM     28     48       1 (Potential).
FT   DOMAIN       49     62       Cytoplasmic (Potential).
FT   TRANSMEM     63     83       2 (Potential).
FT   DOMAIN       84    101       Extracellular (Potential).
FT   TRANSMEM    102    122       3 (Potential).
FT   DOMAIN      123    144       Cytoplasmic (Potential).
FT   TRANSMEM    145    165       4 (Potential).
FT   DOMAIN      166    194       Extracellular (Potential).
FT   TRANSMEM    195    215       5 (Potential).
FT   DOMAIN      216    236       Cytoplasmic (Potential).
FT   TRANSMEM    237    257       6 (Potential).
FT   DOMAIN      258    280       Extracellular (Potential).
FT   TRANSMEM    281    303       7 (Potential).
FT   DOMAIN      304    328       Extracellular (Potential).
FT   DISULFID     99    177       By similarity.
FT   CARBOHYD      5      5       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    173    173       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   328 AA;  36721 MW;  00F9DF5ADADF903E CRC64;

  Query Match             20.4%;  Score 395;  DB 1;  Length 328;
  Best Local Similarity   31.9%;  Pred. No. 4.3e-21;
  Matches  106;  Conservative   55;  Mismatches  137;  Indels   34;  Gaps    9;

Qy         29 MEKVDMNTSQEQGL----CQFSEKYKQVYLSLAYSIIFILGLPLNGTVLWHSWGQTKRWS 84
              ||: |  | |  ||    | : | :|:: |:  ||:: ::|||||  |:       :  :
Db          1 MEQ-DNGTIQAPGLPPTTCVYREDFKRLLLTPVYSVVLVVGLPLNICVIAQICASRRTLT 59

Qy         85 CATTYLVNLMVADLLYVL-LPFLIITYSLDDRWPFGELLCKLVHFLFYINLYGSILLLTC 143
               :  | :|| :|||:|   || ||  |:  | ||||:| |: | |||| ||:|||| |||
Db         60 RSAVYTLNLALADLMYACSLPLLIYNYARGDHWPFGDLACRFVRFLFYANLHGSILFLTC 119

Qy        144 ISVHQFLGVCHPLCSLPYR-TRRHAWLGTSTTWALVVLQLLPTLAFSHTDYINGQMIWYD 202
              ||  ::||:|||| |    |  || ||:     |  | | |||  |: |      : : ||
Db        120 ISFQRYLGICHPLASWHKRGGRRAAWVVCGVVWLAVTAQCLPTAVFAATGIQRNRTVCYD 179

Qy        203 MTSQENFDRLFAYGIVLTLSGFL----SLLGHFGVLFTDGQEPDQARGEPHEDRQHSPSQ 258
              ::       |   ||: ||: |||    :||  :  :       |   |   ::|:   ::
Db        180 LSPPILSTRYLPYGMALTVIGFLLPFIALLACYCRMARRLCRQDGPAGPVAQERRSKAAR 239

Qy        259 VHPDHPTGVWPLHPLFCALPYHSLLLPHHLL-SAFSGLPALDGSQCGLQDMEASGECEQL 317
              :            :  |  :    || |:  :|:  : :  |  | : :  |:
Db        240 M------------AVVVAAVFAISFLPFHITKTAYLAVRSTPGVSCPVLETFAAAYKGTR 287

Qy        318 PQPS------PVLSF----KGGKNRVRLLQKL 339
              |  |      |:| :    |  :    |||:|
Db        288 PFASVNSVLDPILFYFTQQKFRRQPHDLLQRL 319


RESULT 11
AAH64095
ID   AAH64095    PRELIMINARY;      PRT;   328 AA.
AC   AAH64095;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   Pyrimidinergic receptor P2Y, G-protein coupled, 6.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Mammary gland;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Mammary gland;
RA   Strausberg R.;
RL   Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC064095; AAH64095.1; -.
KW   Receptor.
SQ   SEQUENCE   328 AA;  36721 MW;  00F9DF5ADADF903E CRC64;

  Query Match             20.4%;  Score 395;  DB 2;  Length 328;
  Best Local Similarity   31.9%;  Pred. No. 4.3e-21;
  Matches  106;  Conservative   55;  Mismatches  137;  Indels   34;  Gaps    9;

Qy         29 MEKVDMNTSQEQGL----CQFSEKYKQVYLSLAYSIIFILGLPLNGTVLWHSWGQTKRWS 84
              ||: |  | |  ||    | : | :|:: |:  ||:: ::|||||  |:       :  :
Db          1 MEQ-DNGTIQAPGLPPTTCVYREDFKRLLLTPVYSVVLVVGLPLNICVIAQICASRRTLT 59

Qy         85 CATTYLVNLMVADLLYVL-LPFLIITYSLDDRWPFGELLCKLVHFLFYINLYGSILLLTC 143
               :  | :|| :|||:|   || ||  |:  | ||||:| |: | |||| ||:|||| |||
Db         60 RSAVYTLNLALADLMYACSLPLLIYNYARGDHWPFGDLACRFVRFLFYANLHGSILFLTC 119

Qy        144 ISVHQFLGVCHPLCSLPYR-TRRHAWLGTSTTWALVVLQLLPTLAFSHTDYINGQMIWYD 202
              ||  ::||:|||| |    |  || ||:     |  | | |||  |: |      : : ||
Db        120 ISFQRYLGICHPLASWHKRGGRRAAWVVCGVVWLAVTAQCLPTAVFAATGIQRNRTVCYD 179

Qy        203 MTSQENFDRLFAYGIVLTLSGFL----SLLGHFGVLFTDGQEPDQARGEPHEDRQHSPSQ 258
              ::       |   ||: ||: |||    :||  :  :       |   |   ::|:   ::
Db        180 LSPPILSTRYLPYGMALTVIGFLLPFIALLACYCRMARRLCRQDGPAGPVAQERRSKAAR 239

Qy        259 VHPDHPTGVWPLHPLFCALPYHSLLLPHHLL-SAFSGLPALDGSQCGLQDMEASGECEQL 317
              :            :  |  :    || |:  :|:  : :  |  | : :  |:
Db        240 M------------AVVVAAVFAISFLPFHITKTAYLAVRSTPGVSCPVLETFAAAYKGTR 287

Qy        318 PQPS------PVLSF----KGGKNRVRLLQKL 339
              |  |      |:| :    |  :    |||:|
Db        288 PFASVNSVLDPILFYFTQQKFRRQPHDLLQRL 319


RESULT 12
P2Y4_RAT
ID   P2Y4_RAT       STANDARD;      PRT;   361 AA.
AC   O35811;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   P2Y purinoceptor 4 (P2Y4).
GN   Name=P2ry4; Synonyms=P2Y4;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley; TISSUE=Liver;
RA   Bogdanov Y.D., Wildman S., King B.F., Burntock G.;
RL   Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley; TISSUE=Brain;
RX   MEDLINE=98421785; PubMed=9751165;
RA   Webb T.E., Henderson D., Roberts J.A., Barnard E.A.;
RT   "Molecular cloning and characterization of the rat P2Y4 receptor.";
RL   J. Neurochem. 71:1424-1434(1998).
CC   -!- FUNCTION: Receptor for ATP and UTP coupled to G-proteins that
CC       activate a phosphatidylinositol-calcium second messenger system.
CC       Not activated by ADP or UDP.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: Widely expressed at low levels. In brain,
CC       higher expression in the pineal gland and ventricular system.
CC   -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Y14705; CAA75007.1; -.
DR   EMBL; Y11433; CAA72241.1; -.
DR   HSSP; P34996; 1DDD.
DR   RGD; 61798; P2ry4.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR000018; P2Y4_purnocptor.
DR   InterPro; IPR002286; P2_purnocptor.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Glycoprotein; Transmembrane.
FT   DOMAIN        1     30       Extracellular (Potential).
FT   TRANSMEM     31     58       1 (Potential).
FT   DOMAIN       59     68       Cytoplasmic (Potential).
FT   TRANSMEM     69     91       2 (Potential).
FT   DOMAIN       92    108       Extracellular (Potential).
FT   TRANSMEM    109    127       3 (Potential).
FT   DOMAIN      128    149       Cytoplasmic (Potential).
FT   TRANSMEM    150    170       4 (Potential).
FT   DOMAIN      171    192       Extracellular (Potential).
FT   TRANSMEM    193    218       5 (Potential).
FT   DOMAIN      219    242       Cytoplasmic (Potential).
FT   TRANSMEM    243    265       6 (Potential).
FT   DOMAIN      266    283       Extracellular (Potential).
FT   TRANSMEM    284    305       7 (Potential).
FT   DOMAIN      306    361       Cytoplasmic (Potential).
FT   DISULFID    104    181       By similarity.
FT   CARBOHYD    175    175       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   361 AA;  40893 MW;  0377F96E54B449A3 CRC64;

  Query Match             20.0%;  Score 388;  DB 1;  Length 361;
  Best Local Similarity   32.1%;  Pred. No. 1.6e-20;
  Matches  105;  Conservative   54;  Mismatches  126;  Indels   42;  Gaps    9;

Qy         37 SQEQGLCQFSEKYKQVYLSLAYSIIFILGLPLNGTVLWHSWGQTKRWSCATTYLVNLMVA 96
              |   | |:|:|::| : | ::|:::|:||| ||   ||    : : |    ||: :| ::
Db         17 SSGDGDCRFNEEFKFILLPMSYAVVFVLGLALNAPTLWLFLFRLRPWDATATYMFHLALS 76

Qy         97 DLLYVL-LPFLIITYSLDDRWPFGELLCKLVHFLFYINLYGSILLLTCISVHQFLGVCHP 155
              | |||| || |:  |:  : |||| ||| | |||| ||| |:| |||||||::||:|||
Db         77 DTLYVLSLPTLVYYYAARNHWPFGTGLCKFVRFLFYWNLYCSVLFLTCISVHRYLGICHP 136

Qy        156 LCSLPYRTRRHAWLGTSTTWALVVLQLLPTLAFSHTDYINGQMIWYDMTSQENFDR--LF 213
              | :: :   | | |      | :|   |:| | |  |:     :: :| |  | ||    |
Db        137 LRAIRWGRPRFASLLCLGVWLVVAGCLVPNLFFVTTNANGTTILCHDTTLPEEFDHYVYF 196

Qy        214 AYGIVLTLSG--FLSLLGHFGVLFTDGQEPDQARGEPHEDRQHSPSQVHPDHPTGVWPLH 271
              :  ::: | | ||  |  :|::      |    |:       | |::       |
Db        197 SSAVMVLLFGLPFLITLVCYGLMARRLYRPLPGAGQ-------SSSRLRSLRTIAVVLTV 249

Qy        272 PLFCALPYH---SLLLPHHLLSAFSGLPALDGSQCGL----------QDMEASGECEQL 317
              | :|:|   ::     || |          | :           : : ::  |
Db        250 FAVCFVPFHITRTIYYQARLLQA----------DCHVLNIVNVVYKVTRPLASANSC--- 296

Qy        318 PQPSPVL-SFKGGKNRVRLLQKLRQNK 343
                |||  | | | | :| |  | :|
Db        297 --LDPVLYLFTGDKYRNQLQQLCRGSK 321


RESULT 13
P2Y6_HUMAN
ID   P2Y6_HUMAN     STANDARD;      PRT;   328 AA.
AC   Q15077; Q15754;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   P2Y purinoceptor 6 (P2Y6).
GN   Name=P2RY6;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Communi D., Parmentier M., Boeynaems J.M.;
RL   Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97432828; PubMed=9286708;
RA   Somers G.R., Hammet F., Woollatt E., Richards R.I., Southey M.C.,
RA   Venter D.J.;
RT   "Chromosomal localization of the human P2y6 purinoceptor gene and
RT   phylogenetic analysis of the P2y purinoceptor family.";
RL   Genomics 44:127-130(1997).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Placenta;
RX   MEDLINE=97415792; PubMed=9268704;
RA   Maier R., Glatz A., Mosbacher J., Bilbe G.;
RT   "Cloning of P2Y6 cDNAs and identification of a pseudogene: comparison
RT   of P2Y receptor subtype expression in bone and brain tissues.";
RL   Biochem. Biophys. Res. Commun. 237:297-302(1997).
RN   [4]
RP   ERRATUM.
RX   MEDLINE=98069816; PubMed=9412455;
RA   Maier R., Glatz A., Mosbacher J., Bilbe G.;
RL   Biochem. Biophys. Res. Commun. 240:298-302(1997).
RN   [5]
RP   SEQUENCE FROM N.A.
RA   Gu J.R., Wan D.F., Zhao X.T., Zhou X.M., Jiang H.Q., Zhang P.P.,
RA   Qin W.X., Huang Y., Qiu X.K., Qian L.F., He L.P., Li H.N., Yu Y.,
RA   Yu J., Han L.H.;
RT   "Novel human cDNA clones with function of inhibiting cancer cell
RT   growth.";
RL   Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   SEQUENCE FROM N.A.
RA   Puhl H.L. III, Ikeda S.R., Aronstam R.S.;
RT   "cDNA clones of human proteins involved in signal transduction
RT   sequenced by the Guthrie cDNA resource center (www.cdna.org).";
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
RN   [7]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- FUNCTION: Receptor for extracellular UDP > UTP > ATP. The activity
CC       of this receptor is mediated by G proteins which activate a
CC       phosphatidylinositol-calcium second messenger system.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC   ---------------------------------------------------------------------
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CC   use by non-profit institutions as long as its content is in no way
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X97058; CAA65770.1; -.
DR   EMBL; U52464; AAB03572.1; -.
DR   EMBL; AF007892; AAB80713.1; -.
DR   EMBL; AF007891; AAB80712.1; -.
DR   EMBL; AF218005; AAG17247.1; -.
DR   EMBL; AF498920; AAM18129.1; -.
DR   EMBL; BC000571; AAH00571.1; -.
DR   EMBL; BC009391; AAH09391.1; -.
DR   PIR; JC4800; JC4800.
DR   HSSP; P34996; 1DDD.
DR   Genew; HGNC:8543; P2RY6.
DR   MIM; 602451; -.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   GO; GO:0004930; F:G-protein coupled receptor activity; TAS.
DR   GO; GO:0007200; P:G-protein signaling, coupled to IP3 second . . .; TAS.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR001973; P2Y6_purnocptor.
DR   InterPro; IPR002286; P2_purnocptor.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Glycoprotein; Transmembrane.
FT   DOMAIN       1     27       Extracellular (Potential).
FT   TRANSMEM    28     48       1 (Potential).
FT   DOMAIN      49     62       Cytoplasmic (Potential).
FT   TRANSMEM    63     83       2 (Potential).
FT   DOMAIN      84    101       Extracellular (Potential).
FT   TRANSMEM   102    122       3 (Potential).
FT   DOMAIN     123    144       Cytoplasmic (Potential).
FT   TRANSMEM   145    165       4 (Potential).
FT   DOMAIN     166    194       Extracellular (Potential).
FT   TRANSMEM   195    215       5 (Potential).
FT   DOMAIN     216    236       Cytoplasmic (Potential).
FT   TRANSMEM   237    257       6 (Potential).
FT   DOMAIN     258    280       Extracellular (Potential).
FT   TRANSMEM   281    303       7 (Potential).
FT   DOMAIN     304    328       Extracellular (Potential).
FT   CARBOHYD     5      5       N-linked (GlcNAc. . .) (Potential).
FT   DISULFID    99    177       By similarity.
FT   CONFLICT     2      3       Missing (in Ref. 2).
SQ   SEQUENCE   328 AA;  36429 MW;  AAD6C55A43818107 CRC64;

  Query Match             20.0%;  Score 387.5;  DB 1;  Length 328;
  Best Local Similarity   32.7%;  Pred. No. 1.5e-20;
  Matches  108;  Conservative   42;  Mismatches  143;  Indels   37;  Gaps    9;

Qy         33 DMNTSQEQGL----CQFSEKYKQVYLSLAYSIIFILGLPLNGTVLWHSWGQTKRWSCATT 88
              |  | |  ||    | : | :||: |   || :  |||||  |:       :  :
Db          4 DNGTGQALGLPPTTCVYRENFKQLLLPPVYSAVLAAGLPLNICVITQICTSRRALTRTAV 63

Qy         89 YLVNLMVADLLYVL-LPFLIITYSLDDRWPFGELLCKLVHFLFYINLYGSILLLTCISVH 147
              | :|| :|||||   || ||  |:  | ||||:  |:|| |||| ||:|||| |||||
Db         64 YTLNLALADLLYACSLPLLIYNYAQGDHWPFGDFACRLVRFLFYANLHGSILFLTCISFQ 123

Qy        148 QFLGVCHPLCSLPYR-TRRHAWLGTSTTWALVVLQLLPTLAFSHTDYINGQMIWYDMTSQ 206
              ::||:||||     |  || |||     |  |  | |||  |: |     : : ||::
Db        124 RYLGICHPLAPWHKRGGRRAAWLVCVAVWLAVTTQCLPTAIFAATGIQRNRTVCYDLSPP 183

Qy        207 ENFDRLFAYGIVLTLSGFL----SLLGHFGVLFTDGQEPDQARGEPHEDRQHSPSQVHPD 262
                    ||: ||: |||    :||  : :|                  ||  |::
Db        184 ALATHYMPYGMALTVIGFLLPFAALLACYCLLAC-----------RLCRQDGPAEPVAQ 231

Qy        263 HPTGVWPLHPLFCALPYHSLLLPHHLL-SAFSGLPALDGSQCGLQDMEASGECEQLPQP- 320
                 |     :  |  :     || |: :|:  : :  |  | :  :||     :  :|
Db        232 ERRGKAARMAVVVAAAFAISFLPFHITKTAYLAVRSTPGVPCTV--LEAFAAAYKGTRPF 289

Qy        321 -------SPVLSF----KGGKNRVRLLQKL 339
                      |:|:    |  :    |||||
Db        290 ASANSVLDPILFYFTQKKFRRRPHELLQKL 319


RESULT 14
AAP35417
ID   AAP35417    PRELIMINARY;      PRT;   328 AA.
AC   AAP35417;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   Pyrimidinergic receptor P2Y, G-protein coupled, 6.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA   Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
RA   Phelan M., Farmer A.;
RT   "Cloning of human full-length CDSs in BD Creator(TM) System Donor
RT   vector.";
RL   Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BT006771; AAP35417.1; -.
KW   Receptor.
SQ   SEQUENCE   328 AA;  36429 MW;  AAD6C55A43818107 CRC64;

  Query Match             20.0%;  Score 387.5;  DB 2;  Length 328;
  Best Local Similarity   32.7%;  Pred. No. 1.5e-20;
  Matches  108;  Conservative   42;  Mismatches  143;  Indels   37;  Gaps    9;

Qy         33 DMNTSQEQGL----CQFSEKYKQVYLSLAYSIIFILGLPLNGTVLWHSWGQTKRWSCATT 88
              |  | |  ||    | : | :||: |   || :  |||||  |:       :  :
Db          4 DNGTGQALGLPPTTCVYRENFKQLLLPPVYSAVLAAGLPLNICVITQICTSRRALTRTAV 63

Qy         89 YLVNLMVADLLYVL-LPFLIITYSLDDRWPFGELLCKLVHFLFYINLYGSILLLTCISVH 147
              | :|| :|||||   || ||  |:  | ||||:  |:|| |||| ||:|||| |||||
Db         64 YTLNLALADLLYACSLPLLIYNYAQGDHWPFGDFACRLVRFLFYANLHGSILFLTCISFQ 123

Qy        148 QFLGVCHPLCSLPYR-TRRHAWLGTSTTWALVVLQLLPTLAFSHTDYINGQMIWYDMTSQ 206
              ::||:||||     |  || |||     |  |  | |||  |: |     : : ||::
Db        124 RYLGICHPLAPWHKRGGRRAAWLVCVAVWLAVTTQCLPTAIFAATGIQRNRTVCYDLSPP 183
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Qy        207 ENFDRLFAYGIVLTLSGFL----SLLGHFGVLFTDGQEPDQARGEPHEDRQHSPSQVHPD 262
                  ||: ||: |||    :||  : :|                 ||   |::
Db        184 ALATHYMPYGMALTVIGFLLPFAALLACYCLLAC----------RLCRQDGPAEPVAQ 231

Qy        263 HPTGVWPLHPLFCALPYHSLLLPHHLL-SAFSGLPALDGSQCGLQDMEASGECEQLPQP- 320
              |       :  |  :    || |:  :|:  : :  |  | :  :||     :  :|
Db        232 ERRGKAARMAVVVAAAFAISFLPFHITKTAYLAVRSTPGVPCTV--LEAFAAAYKGTRPF 289

Qy        321 -------SPVLSF----KGGKNRVRLLQKL 339
                    |:| :    |  :    |||||
Db        290 ASANSVLDPILFYFTQKKFRRRPHELLQKL 319


RESULT 15
P2Y2_HUMAN
ID   P2Y2_HUMAN     STANDARD;      PRT;   377 AA.
AC   P41231; Q96EM8;
DT   01-FEB-1995 (Rel. 31, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   P2Y purinoceptor 2 (P2Y2) (P2U purinoceptor 1) (P2U1) (ATP receptor)
DE   (Purinergic receptor).
GN   Name=P2RY2; Synonyms=P2RU1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Airway epithelium;
RX   MEDLINE=94211846; PubMed=8159738;
RA   Parr C.E., Sullivan D.M., Paradiso A.M., Lazarowski E.R., Burch L.H.,
RA   Olsen J.C., Erb L., Weisman G.A., Boucher R.C., Turner J.T.;
RT   "Cloning and expression of a human P2U nucleotide receptor, a target
RT   for cystic fibrosis pharmacotherapy.";
RL   Proc. Natl. Acad. Sci. U.S.A. 91:3275-3279(1994).
RN   [2]
RP   REVISIONS.
RX   MEDLINE=95108098; PubMed=7809171;
RA   Parr C.E., Sullivan D.M., Paradiso A.M., Lazarowski E.R., Burch L.H.,
RA   Olsen J.C., Erb L., Weisman G.A., Boucher R.C., Turner J.T.;
RT   "Cloning and expression of a human P2U nucleotide receptor, a target
RT   for cystic fibrosis pharmacotherapy.";
RL   Proc. Natl. Acad. Sci. U.S.A. 91:13067-13067(1994).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Placenta;
RA   Puhl H.L. III, Ikeda S.R., Aronstam R.S.;
RT   "cDNA clones of human proteins involved in signal transduction
RT   sequenced by the Guthrie cDNA resource center (www.cdna.org).";
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney, and Leukocyte;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- FUNCTION: Receptor for ATP and UTP coupled to G-proteins that
CC       activate a phosphatidylinositol-calcium second messenger system.
CC       The affinity range is UTP = ATP > ATP-gamma-S >> 2-methylthio-ATP
CC       = ADP.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: Spleen, testis, kidney, liver, lung, heart and
CC       brain.
CC   -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U07225; AAC04923.1; -.
DR   EMBL; AY136753; AAN01279.1; -.
DR   EMBL; BC012104; AAH12104.1; -.
DR   EMBL; BC028135; AAH28135.1; -.
DR   HSSP; P34996; 1DDD.
DR   Genew; HGNC:8541; P2RY2.
DR   MIM; 600041; -.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   GO; GO:0004872; F:receptor activity; TAS.
DR   GO; GO:0006873; P:cell ion homeostasis; TAS.
DR   GO; GO:0007200; P:G-protein signaling, coupled to IP3 second . . .; TAS.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR000356; P2U_purnocptor.
DR   InterPro; IPR002286; P2_purnocptor.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Glycoprotein; Transmembrane.
FT   DOMAIN       1     32       Extracellular (Potential).
FT   TRANSMEM     33    59       1 (Potential).
FT   DOMAIN       60    70       Cytoplasmic (Potential).
FT   TRANSMEM     71    93       2 (Potential).
FT   DOMAIN       94    110      Extracellular (Potential).
FT   TRANSMEM     111   129      3 (Potential).
FT   DOMAIN       130   152      Cytoplasmic (Potential).
FT   TRANSMEM     153   172      4 (Potential).
FT   DOMAIN       173   194      Extracellular (Potential).
FT   TRANSMEM     195   220      5 (Potential).
FT   DOMAIN       221   246      Cytoplasmic (Potential).
FT   TRANSMEM     247   269      6 (Potential).
FT   DOMAIN       270   287      Extracellular (Potential).
FT   TRANSMEM     288   309      7 (Potential).
FT   DOMAIN       310   377      Cytoplasmic (Potential).
FT   CARBOHYD     9     9        N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     13    13       N-linked (GlcNAc. . .) (Potential).
FT   DISULFID     106   183      By similarity.
FT   CONFLICT     312   312      R -> S (in Ref. 4; AAH12104).
FT   CONFLICT     350   350      E -> G (in Ref. 1).
FT   CONFLICT     359   359      S -> F (in Ref. 1).
SQ   SEQUENCE   377 AA;  42289 MW;  EE557A857A269AC6 CRC64;

  Query Match           20.0%;  Score 387.5;  DB 1;  Length 377;
  Best Local Similarity  32.7%;  Pred. No. 1.8e-20;
  Matches  117;  Conservative   41;  Mismatches  119;  Indels   81;  Gaps   13;

Qy         43 CQFSEKYKQVYLSLAYSIIFILGLPLNGTVLWHSWGQTKRWSCATTYLVNLMVADLLYVL 102
              |:|:| :| | | ::| :: :||| ||   |:    : | |: :|||: :| |:| ||
Db         25 CRFNEDFKYVLLPVSYGVVCVLGLCLNAVALYIFLCRLKTWNASTTYMFHLAVSDALYAA 84

Qy        103 -LPFLIITYSLDDRWPFGELLCKLVHFLFYINLYGSILLLTCISVHQFLGVCHPLCSLPY 161
               || |:  |:  | |||  :||||| |||| ||| ||| ||||||: |||  || || :
Db         85 SLPLLVYYYARGDHWPFSTVLCKLVRFLFYTNLYCSILFLTCISVHRCLGVLRPLRSLRW 144
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Qy        162 RTRRHAWLGTSTTWALVVLQLLPTLAFSHTDYINGQMIWYDMTSQENFDRLFAYGIVLTL 221
Db        145 GRARYARRVAGAVWVLVLACQAPVLYFVTTSARGGRVTCHDTSAPELFSRFVAYSSVM-- 202

Qy        222 SGFLSLLGHFGVLF--------------------TDGQEPDQARGEPHEDRQHSPSQVHP 261
Db        203 ---LGLL--FAVPFAVILVCYVLMARRLLKPAYGTSG-------GLPRAKRKSVRT---- 246

Qy        262 DHPTGVWPLHPLF--CALPYH----------SLLLPHHLLSAFS-----GLPALDGSQCG 304
Db        247 -----IAVVLAVFALCFLPFHVTRTLYYSFRSLDLSCHTLNAINMAYKVTRPLASANSC- 300

Qy        305 LQDMEASGECEQLPQPSPVLSFKGGKNRVRLLQKLRQNKLGEHPA--GRKRCPGLNRS 360
Db        301 --------------LDPVLYFLAGQRLVRFARDAKP-PTGPSPATPARRRL-GLRRS 341
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Search completed: November 4, 2004, 17:01:16
Job time : 194 secs